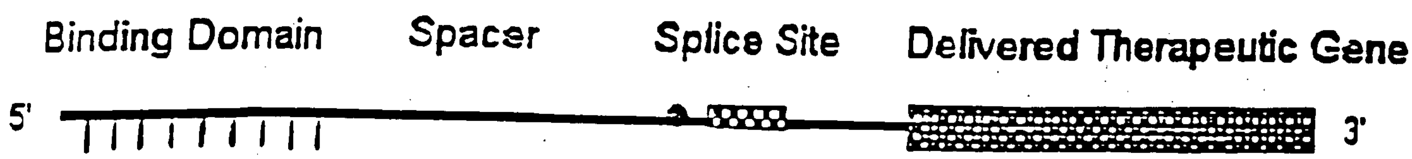
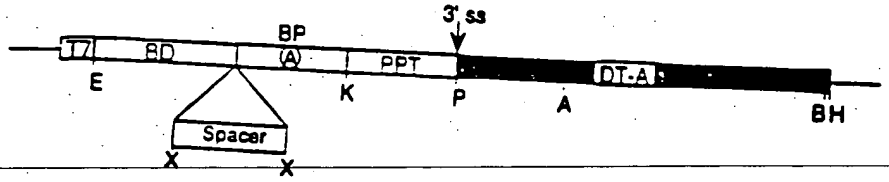
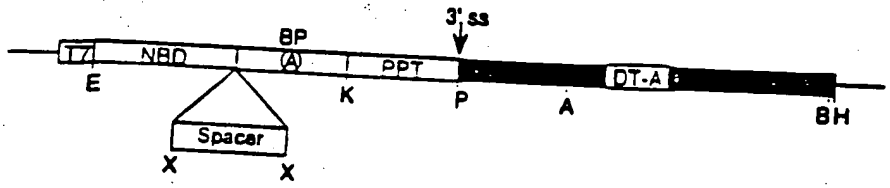
FIGURE 1A


Binding Domain
Spacer
Splice Site
Delivered Therapeutic Gene
5'
3'

(B) (1) pPTM+Sp



(2) pPTM-Sp



(C)

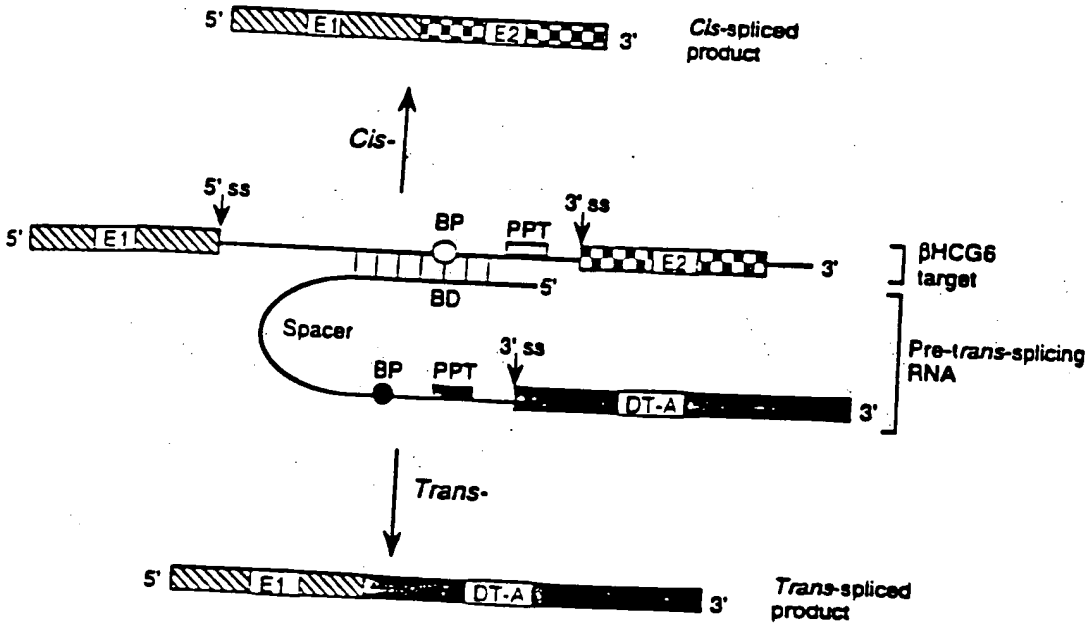
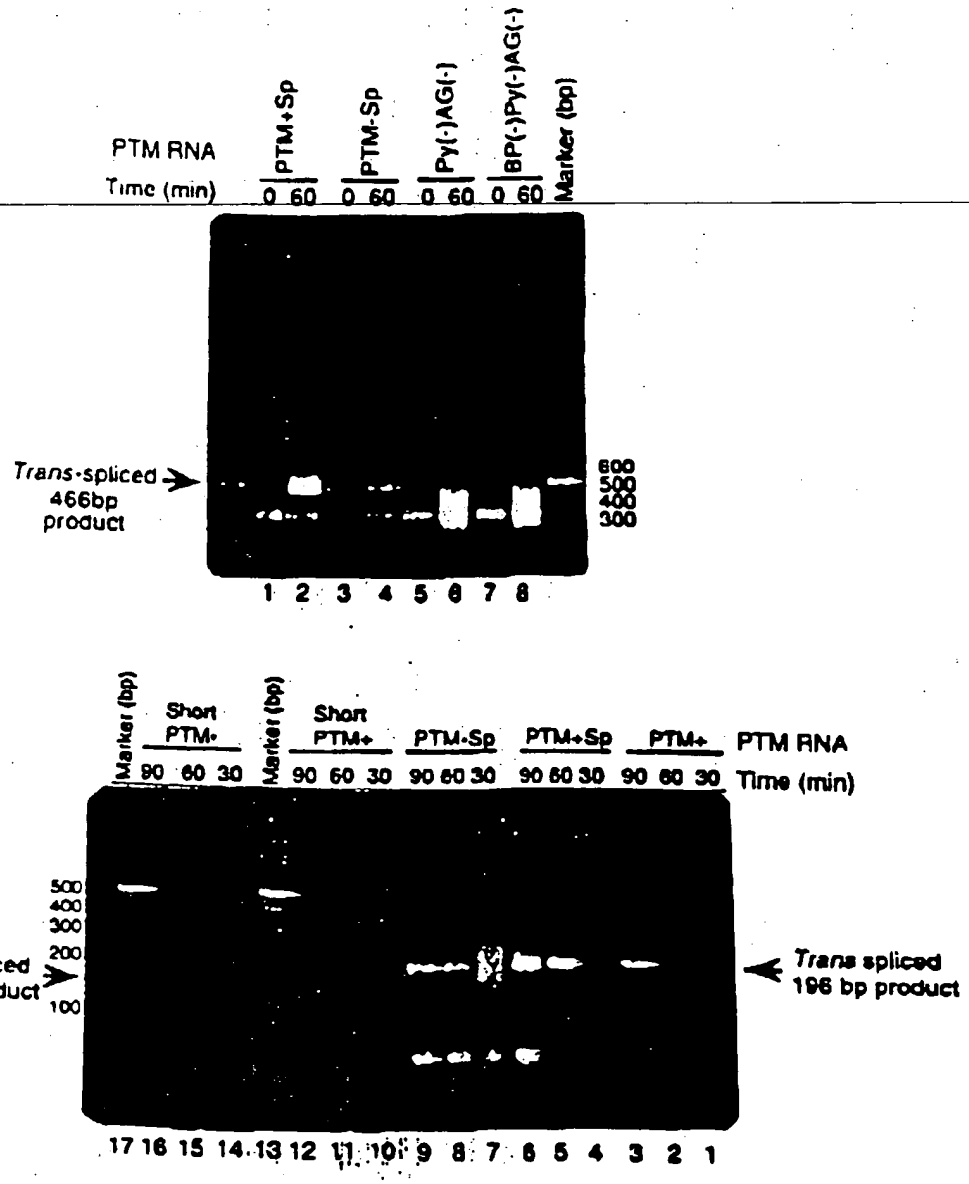
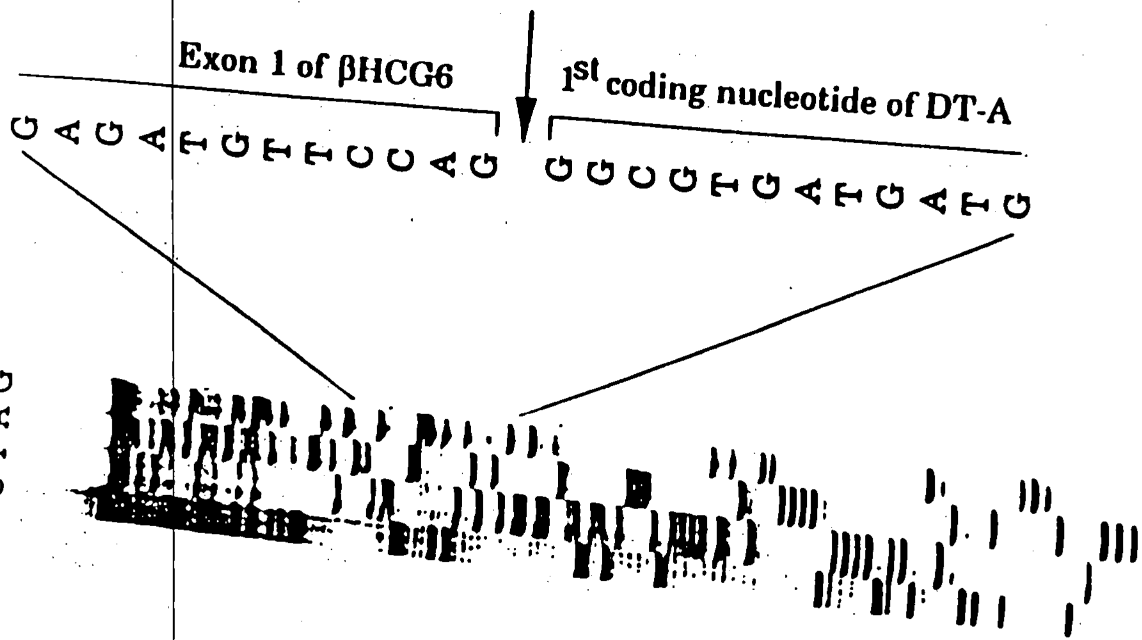
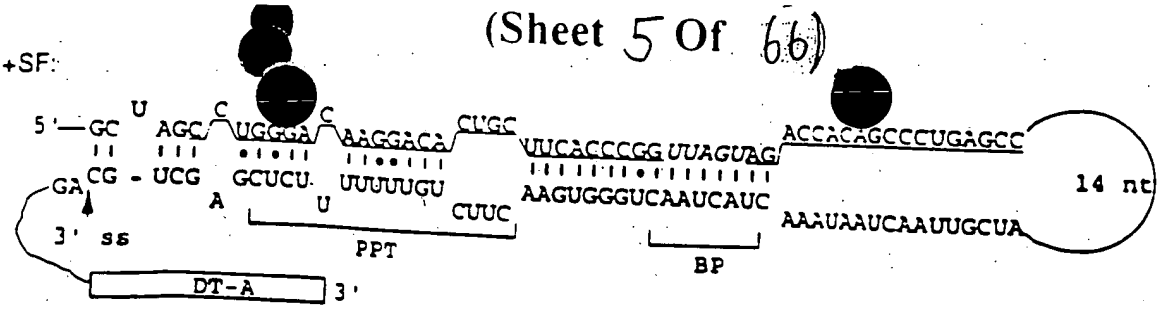


Figure 1B-C

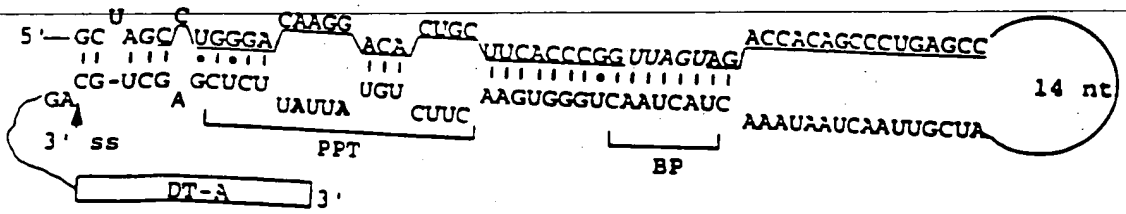

A
PTM RNA
Time (min)
PTM+Sp
PTM-Sp
Py(-)AG(-)
BP(-)Py(-)AG(-)
Marker (bp)
0 60 0 60 0 60 0 60
Trans-spliced
466bp
product
600
500
400
300
1 2 3 4 5 6 7 8
B
Marker (bp)
Short
PTM-
Marker (bp)
Short
PTM+
PTM-Sp
PTM+Sp
PTM+
PTM RNA
90 60 30 90 60 30 90 60 30 90 60 30 90 60 30
Time (min)
500
400
300
200
100
Trans spliced
143 bp product
Trans spliced
196 bp product
17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1


Exon 1 of βHCG6
1st coding nucleotide of DT-A
G A G A T G T T C C A G
G G C G T G A T G A T G
C T A G

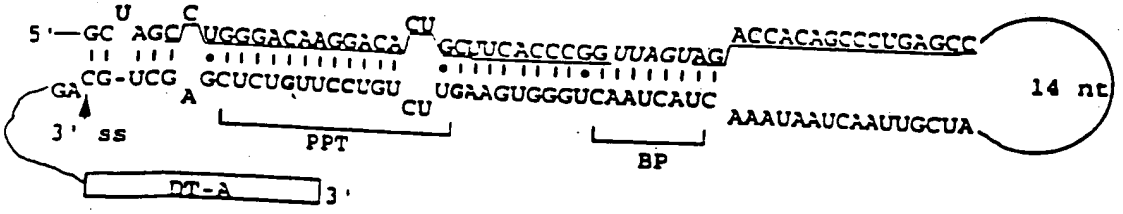
1. PTM+SF:



2. PTM+SF-Py1:



3. PTM+SF-Py2:



(B)

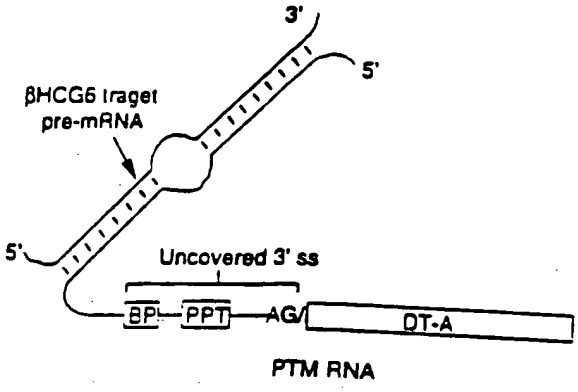


Figure 4A-B

(C)

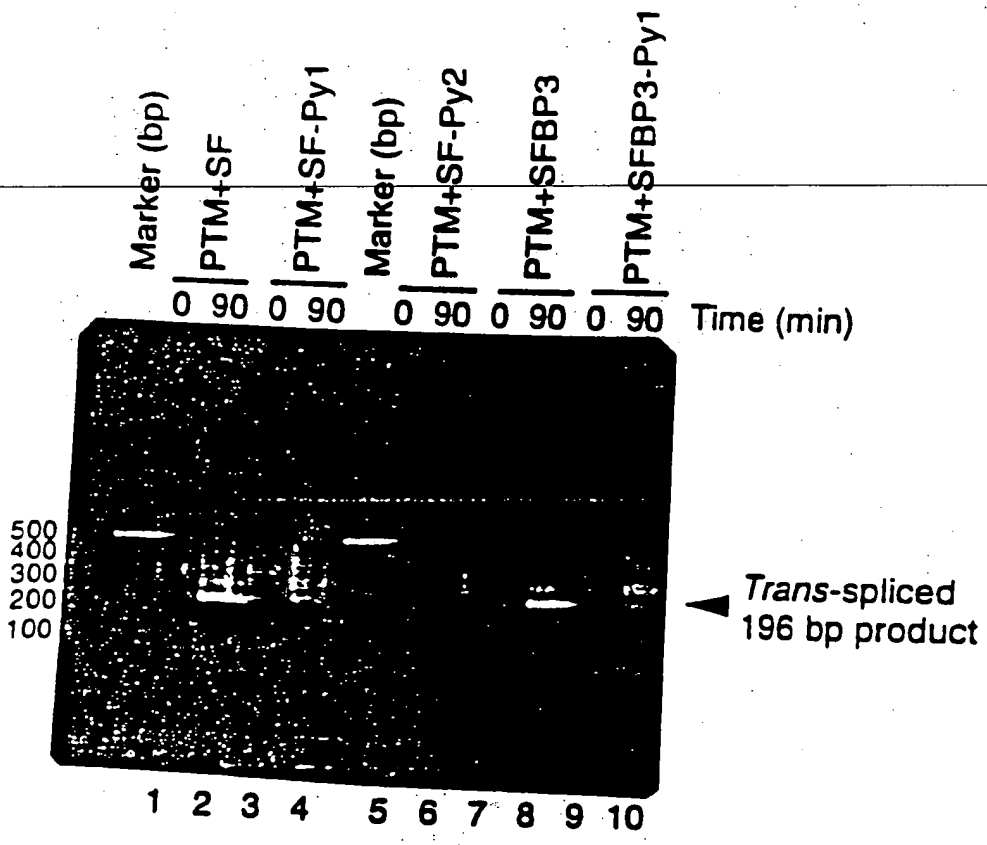

Marker (bp)
PTM+SF
PTM+SF-Py1
Marker (bp)
PTM+SF-Py2
PTM+SFBP3
PTM+SFBP3-Py1
0 90 0 90 0 90 0 90 0 90
Time (min)
500
400
300
200
100
Trans-spliced
196 bp product
1 2 3 4 5 6 7 8 9 10

Figure 4C

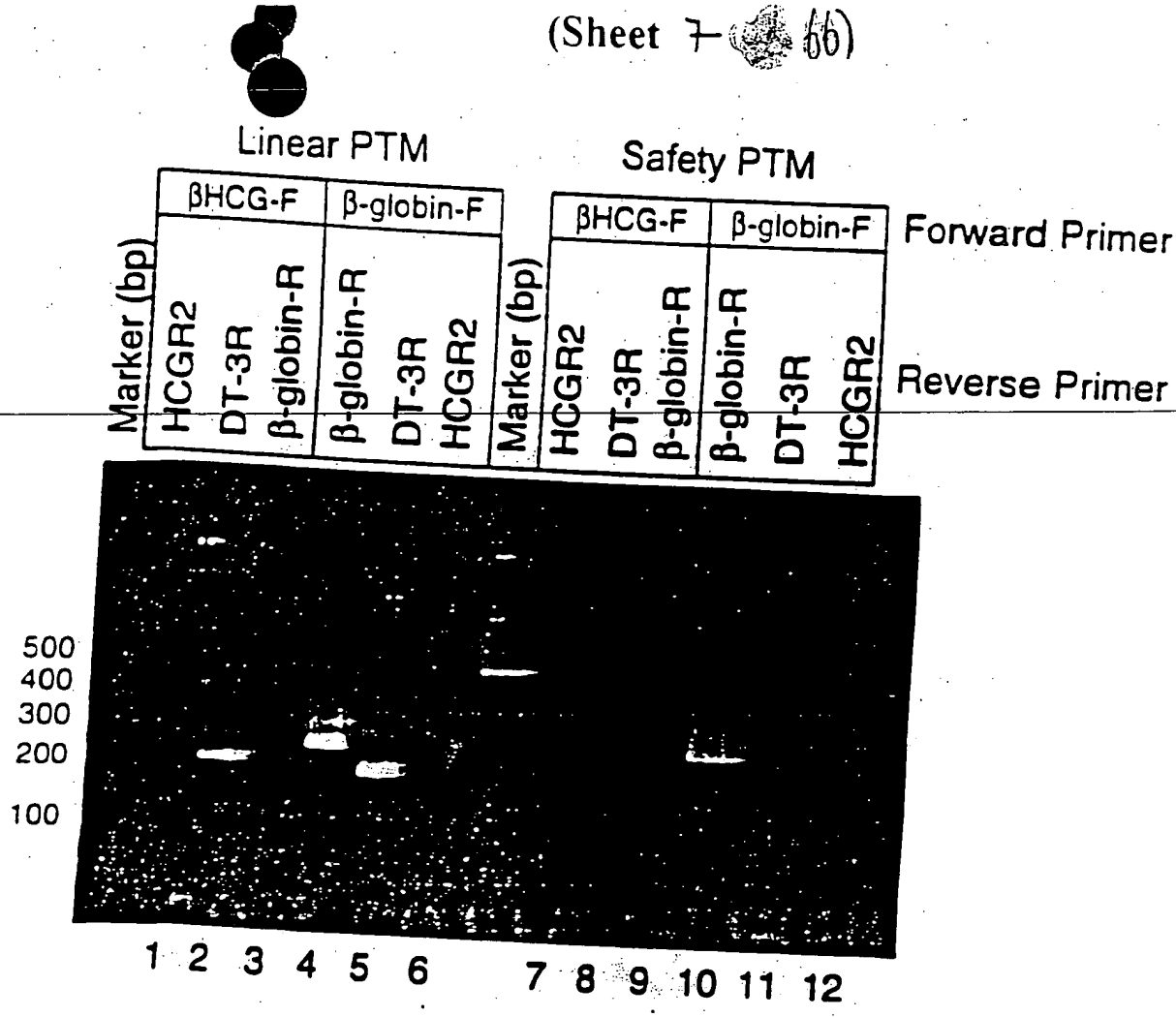

Linear PTM
Safety PTM
βHCG-F
β-globin-F
βHCG-F
β-globin-F
Forward Primer
Marker (bp)
HCGR2
DT-3R
β-globin-R
β-globin-R
DT-3R
HCGR2
Marker (bp)
HCGR2
DT-3R
β-globin-R
β-globin-R
DT-3R
HCGR2
Reverse Primer
500
400
300
200
100
1 2 3 4 5 6 7 8 9 10 11 12

Figure 5

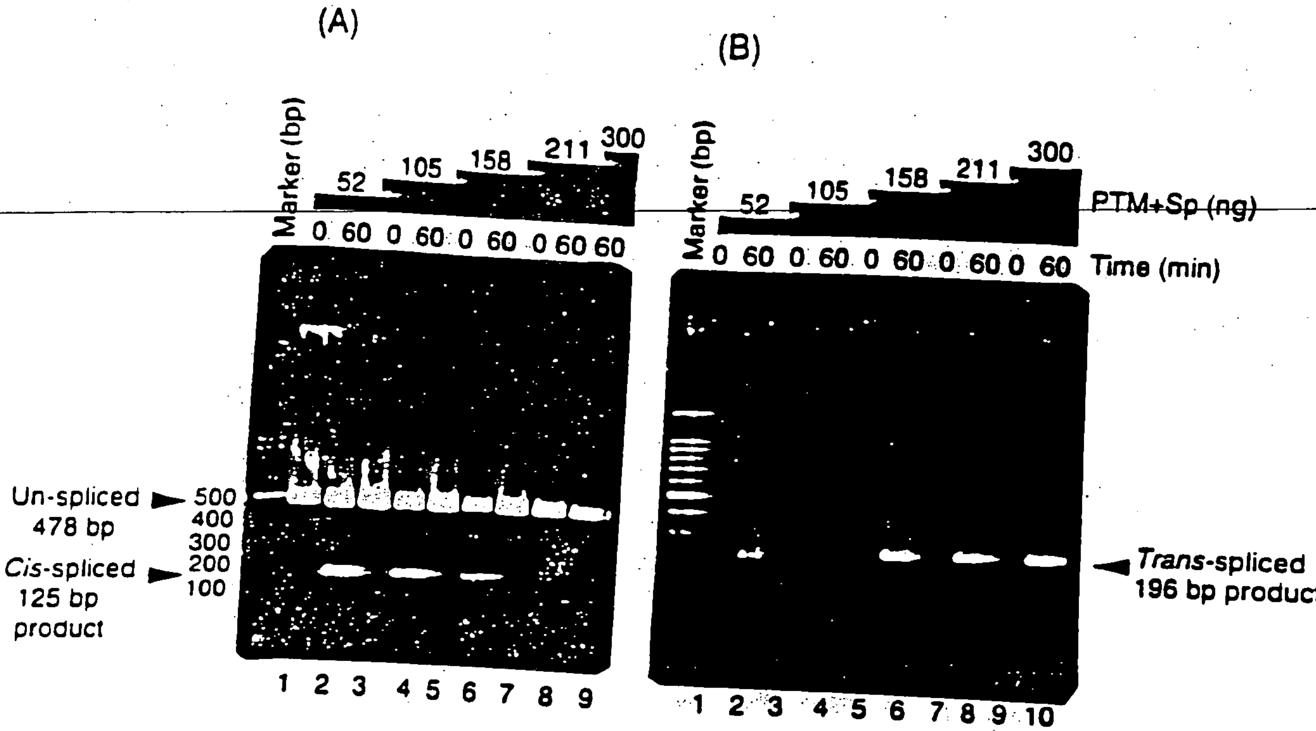
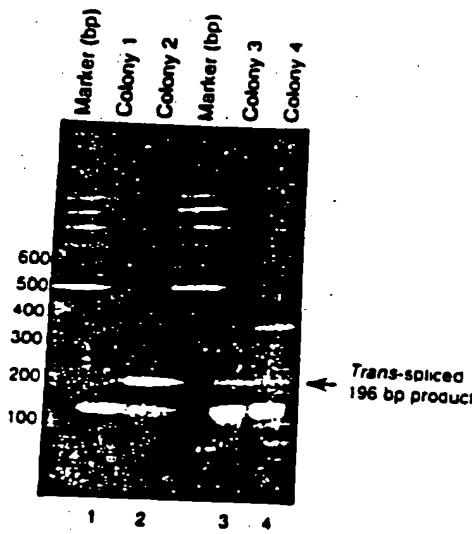

(A)
(B)
Marker (bp)
52
105
158
211
300
PTM+Sp (ng)
0 60 0 60 0 60 0 60 60
0 60 0 60 0 60 0 60 0 60
Time (min)
Un-spliced 478 bp
500
400
300
200
100
Cis-spliced 125 bp product
Trans-spliced 196 bp product
1 2 3 4 5 6 7 8 9
1 2 3 4 5 6 7 8 9 10

Figure6

Figure 7

(A)



(B)

Exon 1 of βHCG6 ↓

5'-<u>CAGGGGACGCACCAAGGATGGAGATGTTCCAG</u>-GGCGCTGATGATGTTGTT

↑ 1st coding nucleotide of DT-A

GATTCTTCTTAAATCTTTTGTGATGGAAAACTTTTCTTCGTACCACGGGACTA

AACCTGGTTATGTAGATTCCATTCAAAAA-3'

Double Splicing Pre-therapeutic RNA

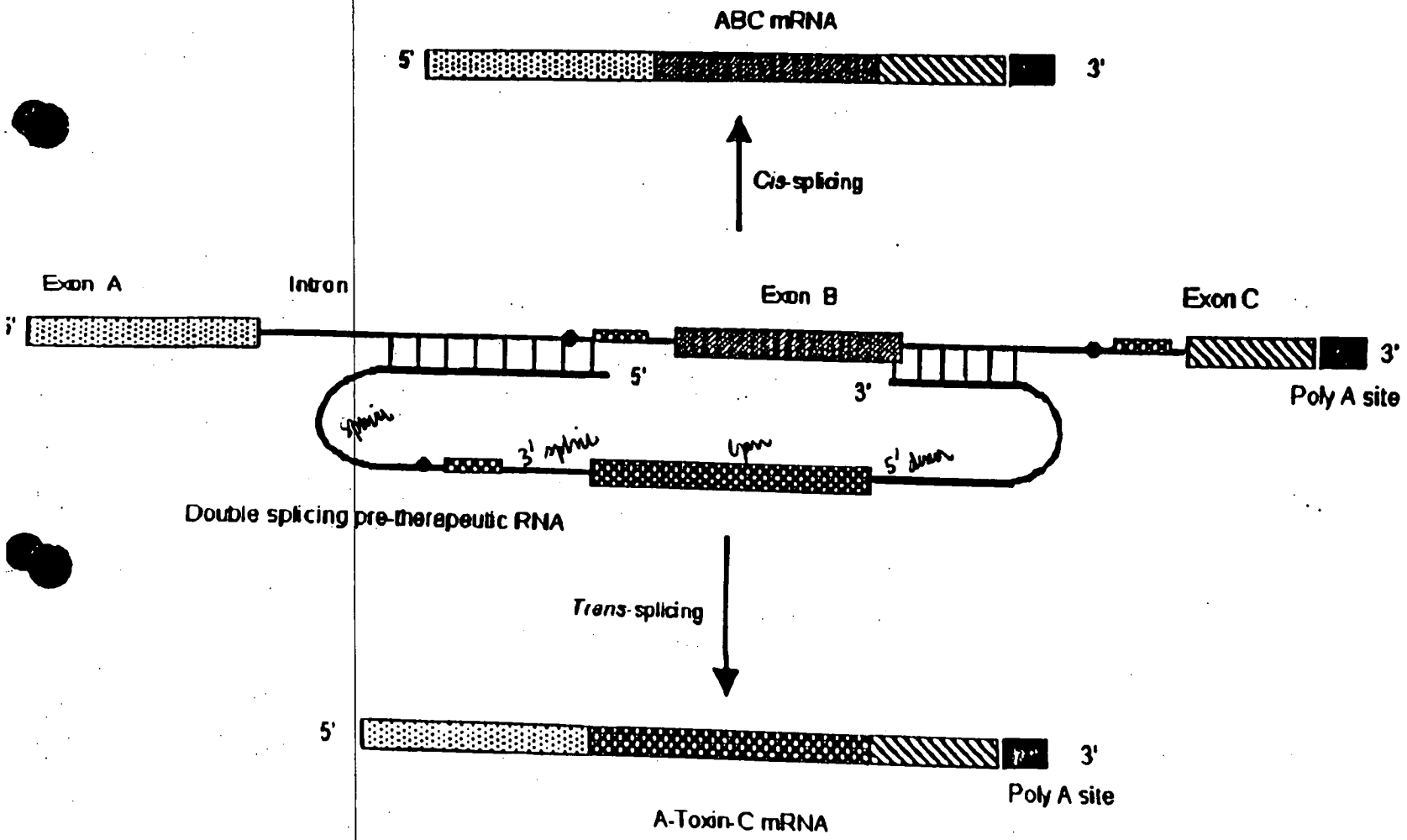


Figure 8A

31304B-A

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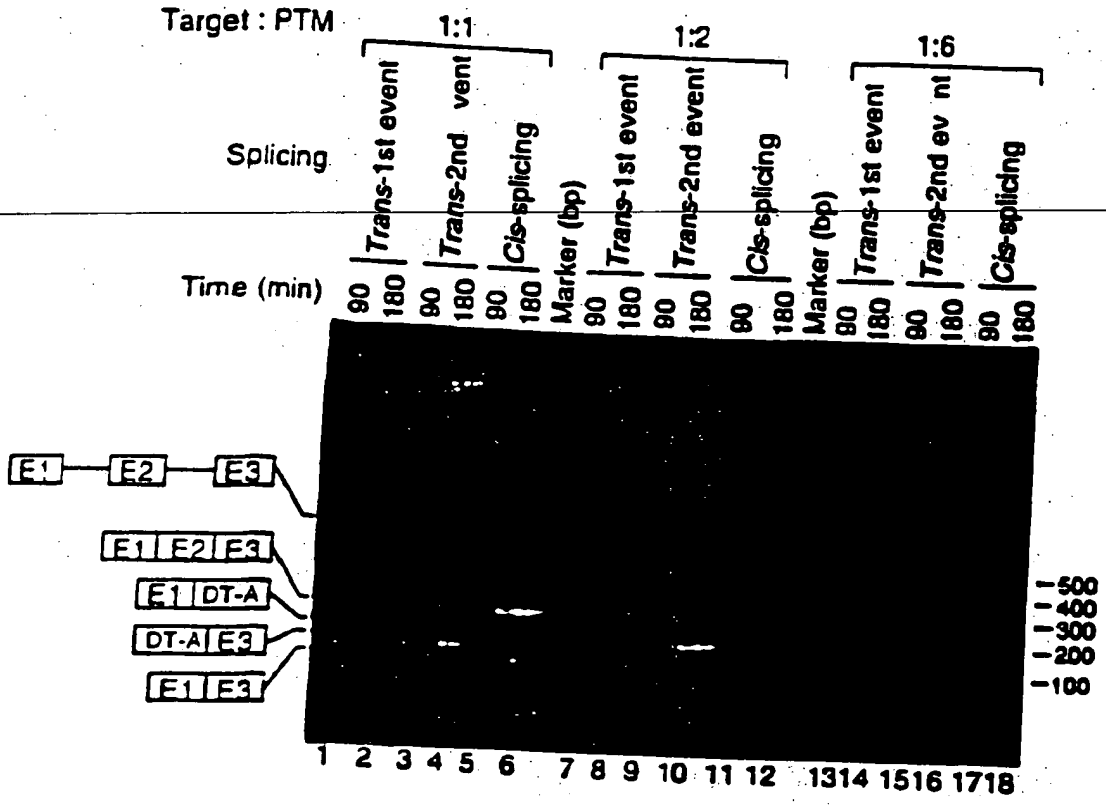
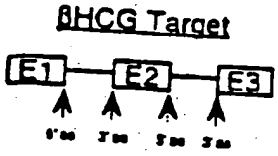
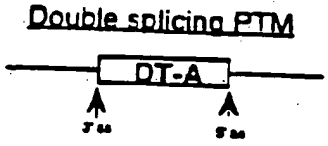
Sele[redacted] *Trans*-splicing of a Double Spli[redacted] PTM

(3' ss o[redacted]TM to 5' ss target and, 5' ss of PTM to 3' ss of target)







Cis-spliced products

E1 E2 E3 = Normal *cis*-splicing (277bp)

E1 E3 = Exon skipping (110bp)

Trans-splicied products

E1 DT-A = 1st event, 196bp. *Trans*-splicing between 5' ss of target & 3' ss of PTM.

DT-A E3 = 2nd event, 161bp. *Trans*-splicing between 3' ss of target & 5' ss of PTM.

Figure 8B

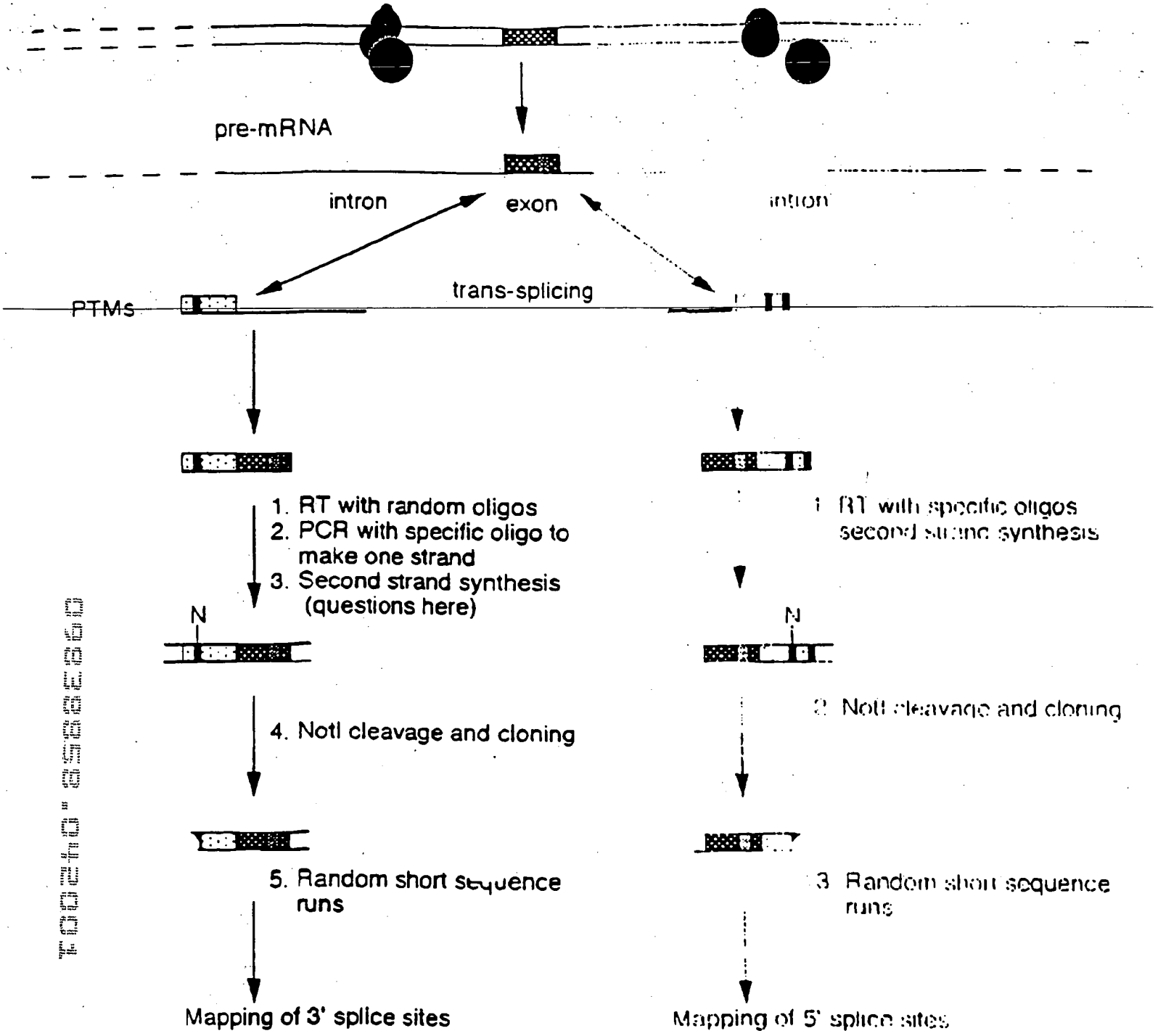
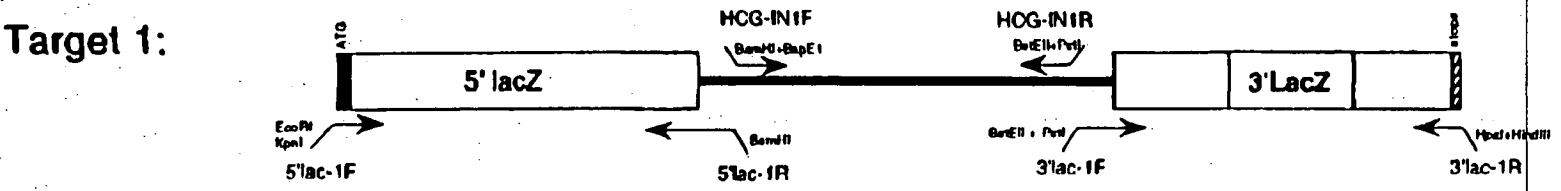

pre-mRNA
intron
exon
intron
PTMs
trans-splicing
1. RT with random oligos
2. PCR with specific oligo to make one strand
3. Second strand synthesis (questions here)
N
4. NotI cleavage and cloning
5. Random short sequence runs
Mapping of 3' splice sites
1. RT with specific oligos
second strand synthesis
N
2. NotI cleavage and cloning
3. Random short sequence runs
Mapping of 5' splice sites

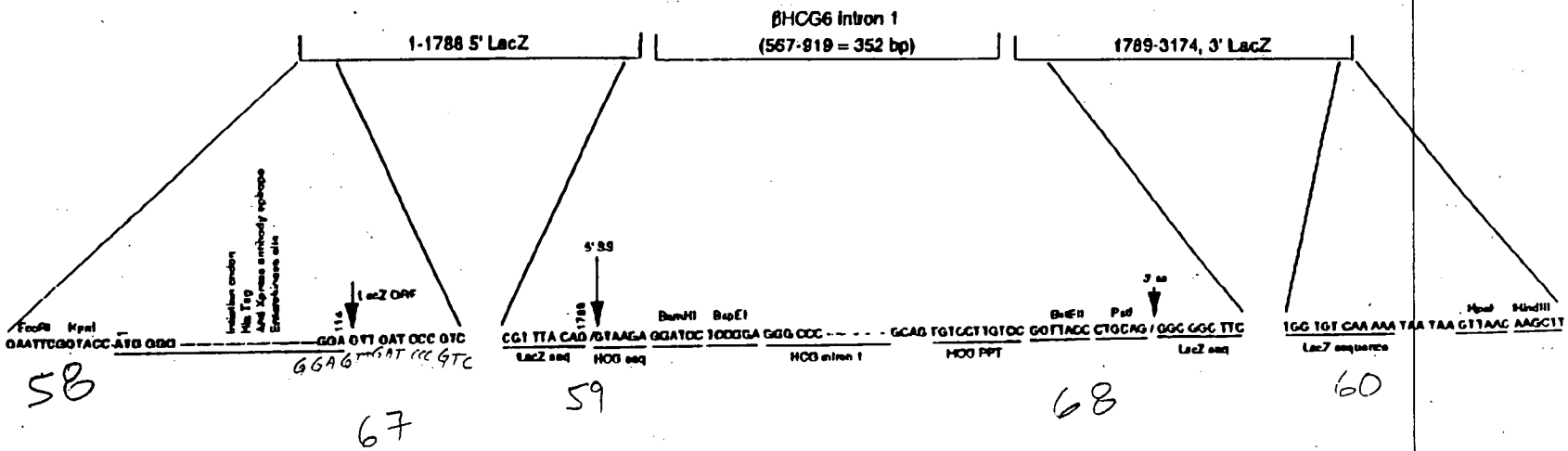
FIGURE 9

LacZ Knock Out Model Constructs

pc3·1 Lac-T1

Target 1:





PTMs

pc3·1PTM2 :-

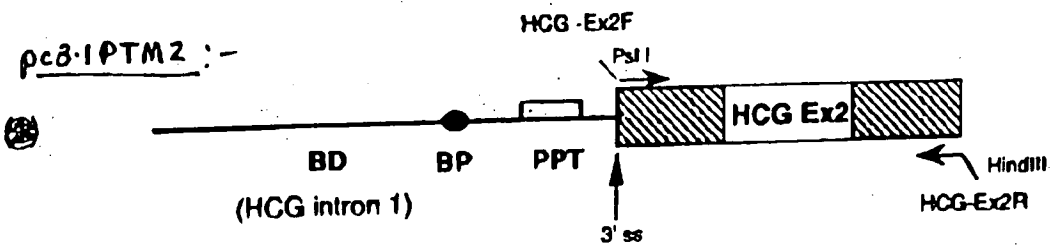


FIG. 10A (sheet 13 of 66)

Restoration of β-Gal activity by SMaRT

(Spliceosome Mediated RNA*Trans*-splicing)

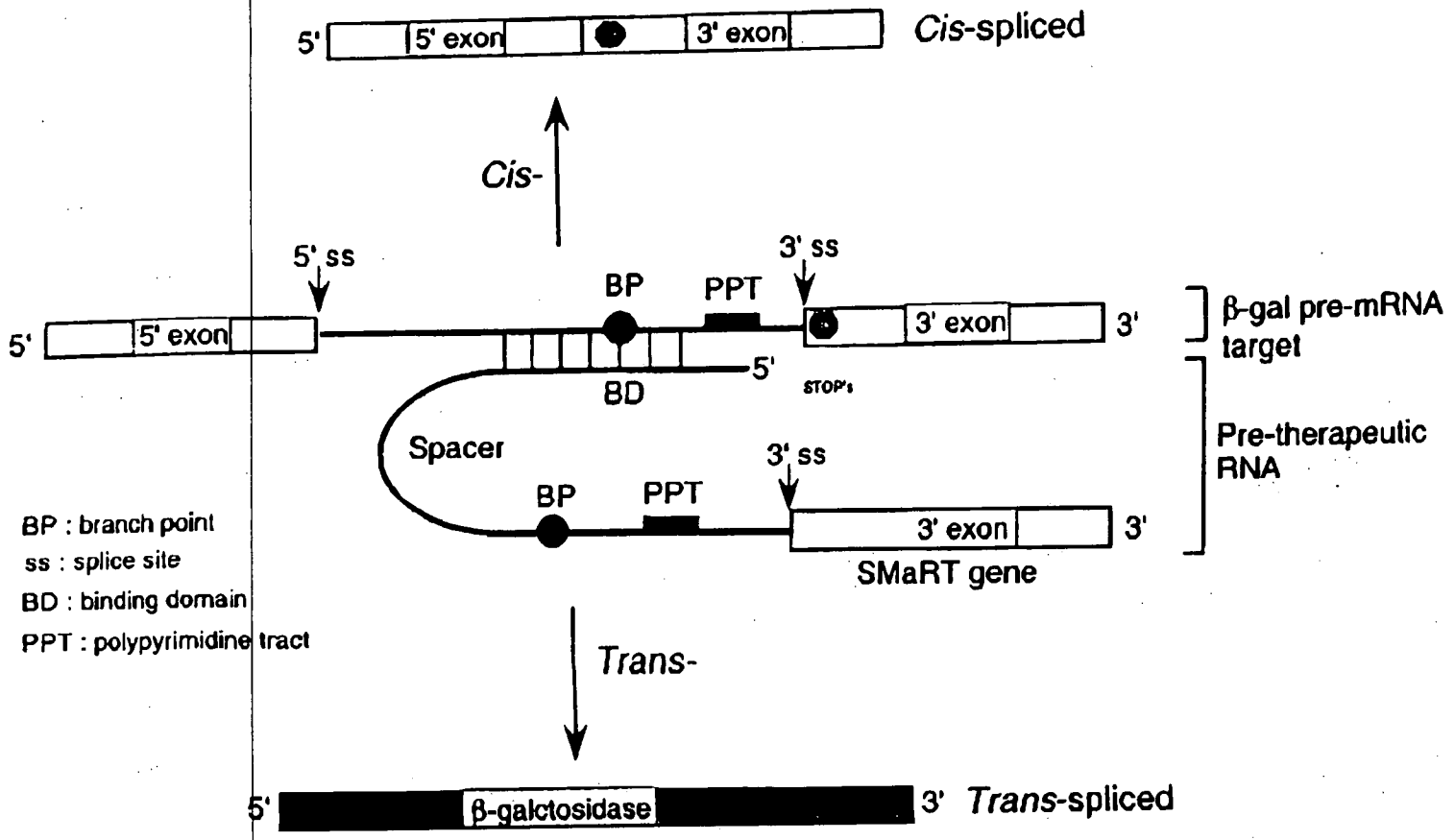


Figure 1D B

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(Amt 14 of 661)

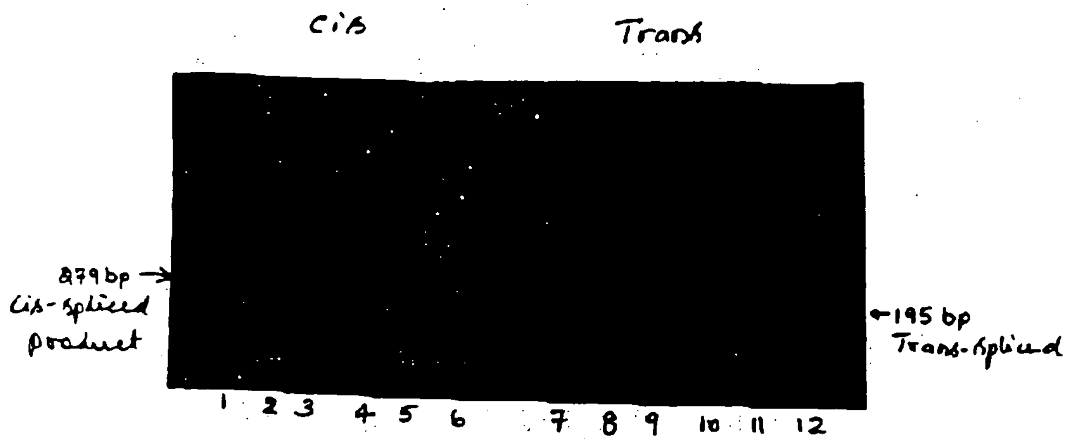

Cis
Trans
879 bp
Cis-spliced product
←195 bp
Trans-spliced
1
2
3
4
5
6
7
8
9
10
11
12

FIGURE 11A

(Sheet 16 of 66)

Figure 11B

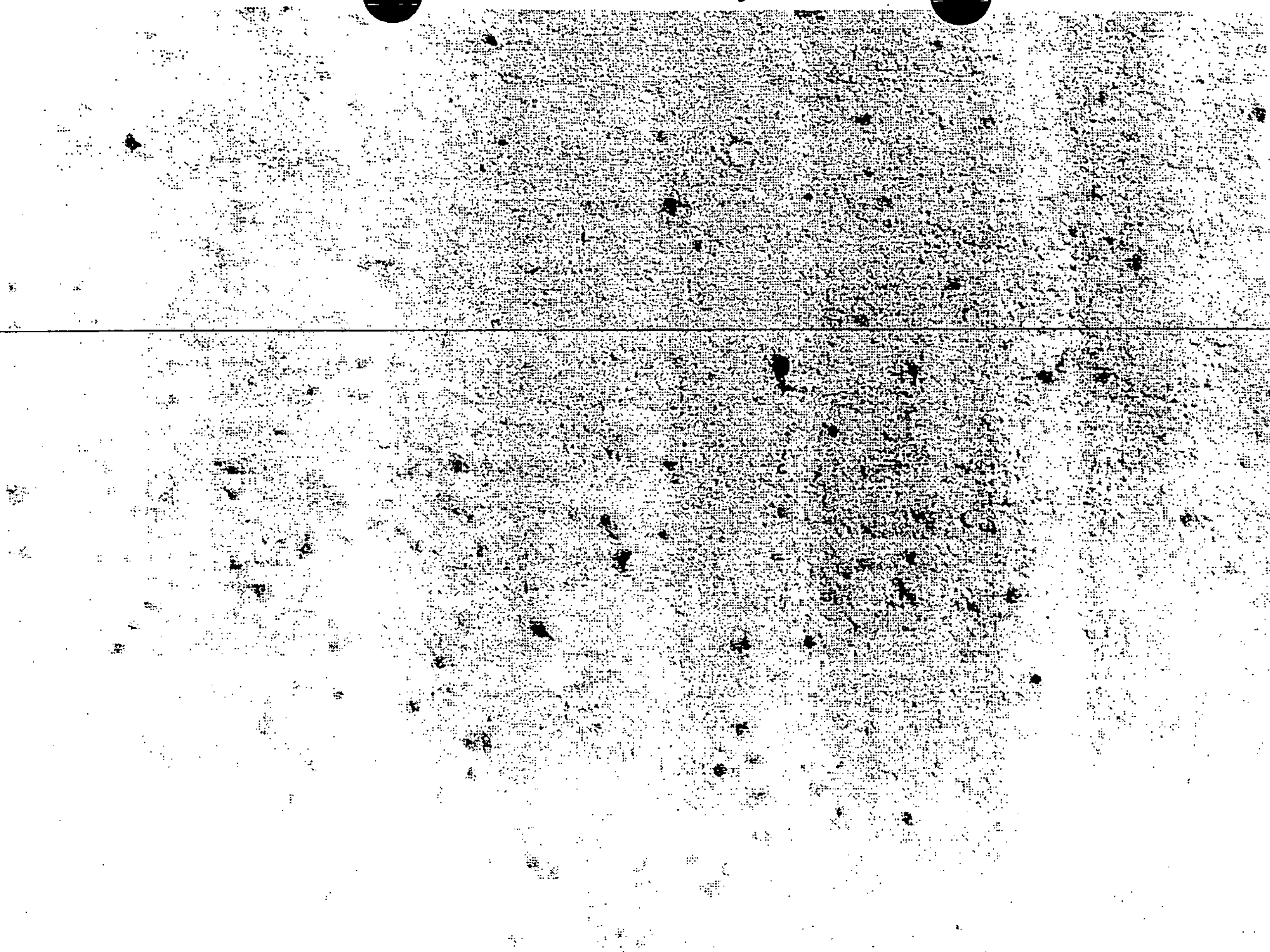


FIGURE 11C

Nucleotide Sequence Demonstrating that *Trans*-splicing is Accurate

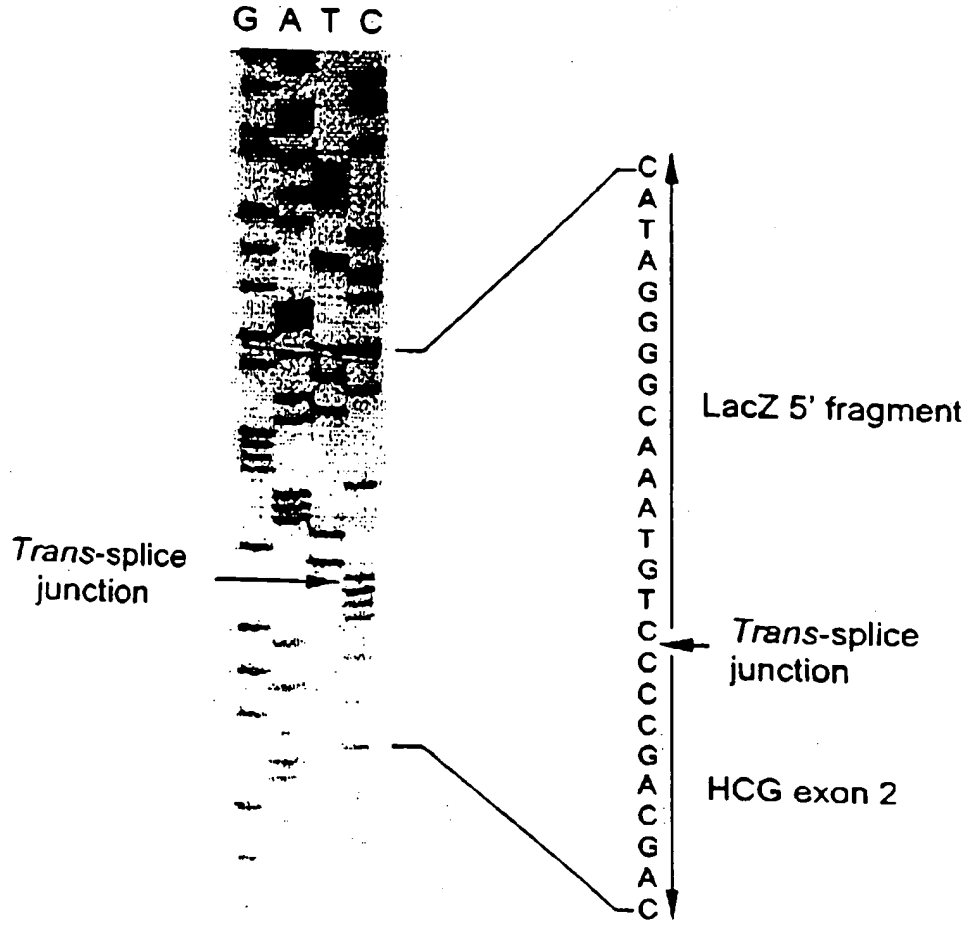


FIGURE 12A

31304-B-A

(Sheet 18 of 66)

(1). Nucleotide sequences of the *cis*-spliced product (285 bp) :

BioLac-TR1
GGCTTTCGCTACCTGGAGAGACGCGCCCGCTGATCCTTTGCGAATACGCCCACGCGATGGGTAACAGTCTTG

Splice junction
GCGGTTTCGCTAAATACTGGCAGGCGTTTCGTCAGTATCCCCGTTTACAG/GGCGGCTTCGTCTAATAATG

GGACTGGGTGGATCAGTCGCTGATTAAATATGATGAAAACGGCAACCCGTGGTCGGCTTACGGCGGTGATTT

Lac-TR2
TGGCGATACGCCGAACGATCGCCAGTTCTGTATGAACGGTCTGGTCTTTGGCGACCGCACGCCGCATCCAG

(2) Nucleotide sequences of the trans-spliced product (195 bp)

BioLac-TR1
GGCTTTCGCTACCTGGAGAGACGCGCCCGCTGATCCTTTGCGAATACGCCCACGCGATGGGTAACAGTCTTGG

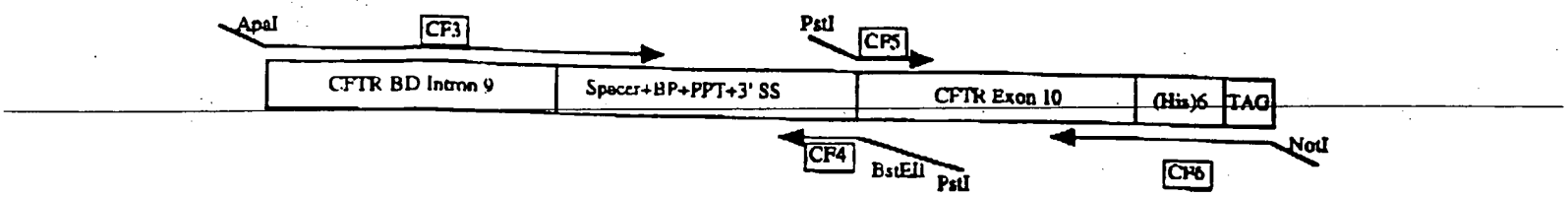
Splice junction
CGGTTTCGCTAAATACTGGCAGGCGTTTCGTCAGTATCCCCGTTTACAG/GGGCTGCTGCTGTTGCTGCTGCT

HCGR2
GAGCATGGGCGGGACATGGGCATCCAAGGAGCCACTTCGGCCACGGTGCCG

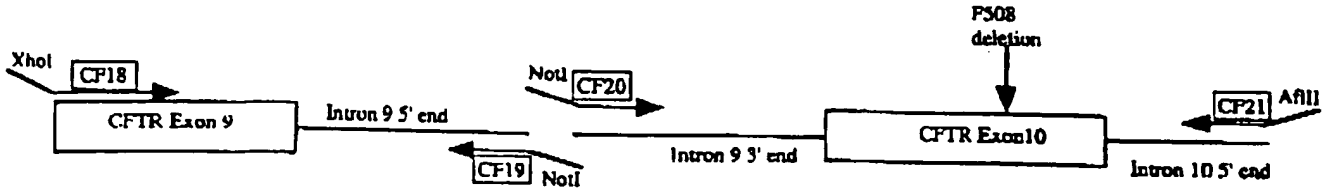
Figure 12 B

31304-B-A
(Shut 19 of 66)

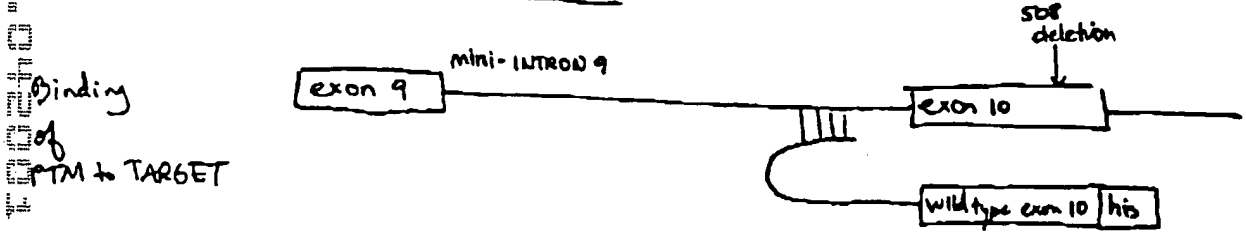
CFTR Pre-therapeutic molecule (PTM or "bullet")



CFTR mini-gene target - Construction



TRANS-SPLICING Repair



↓ splicing

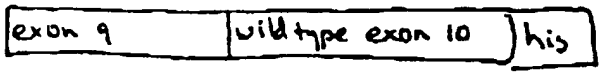
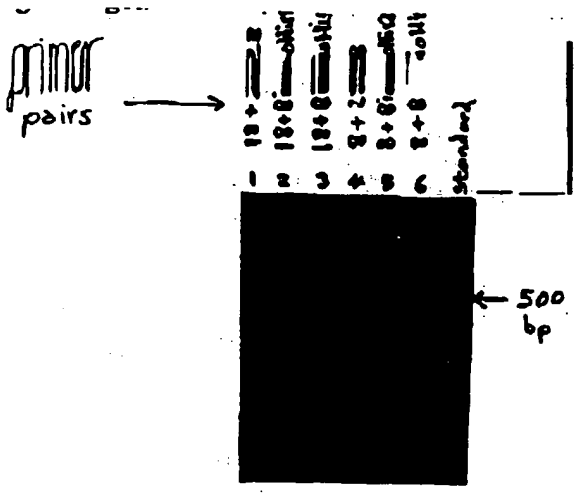


Figure 13

31304-B-A
(Shut 2004 66)

Figure 14



31304 B-A
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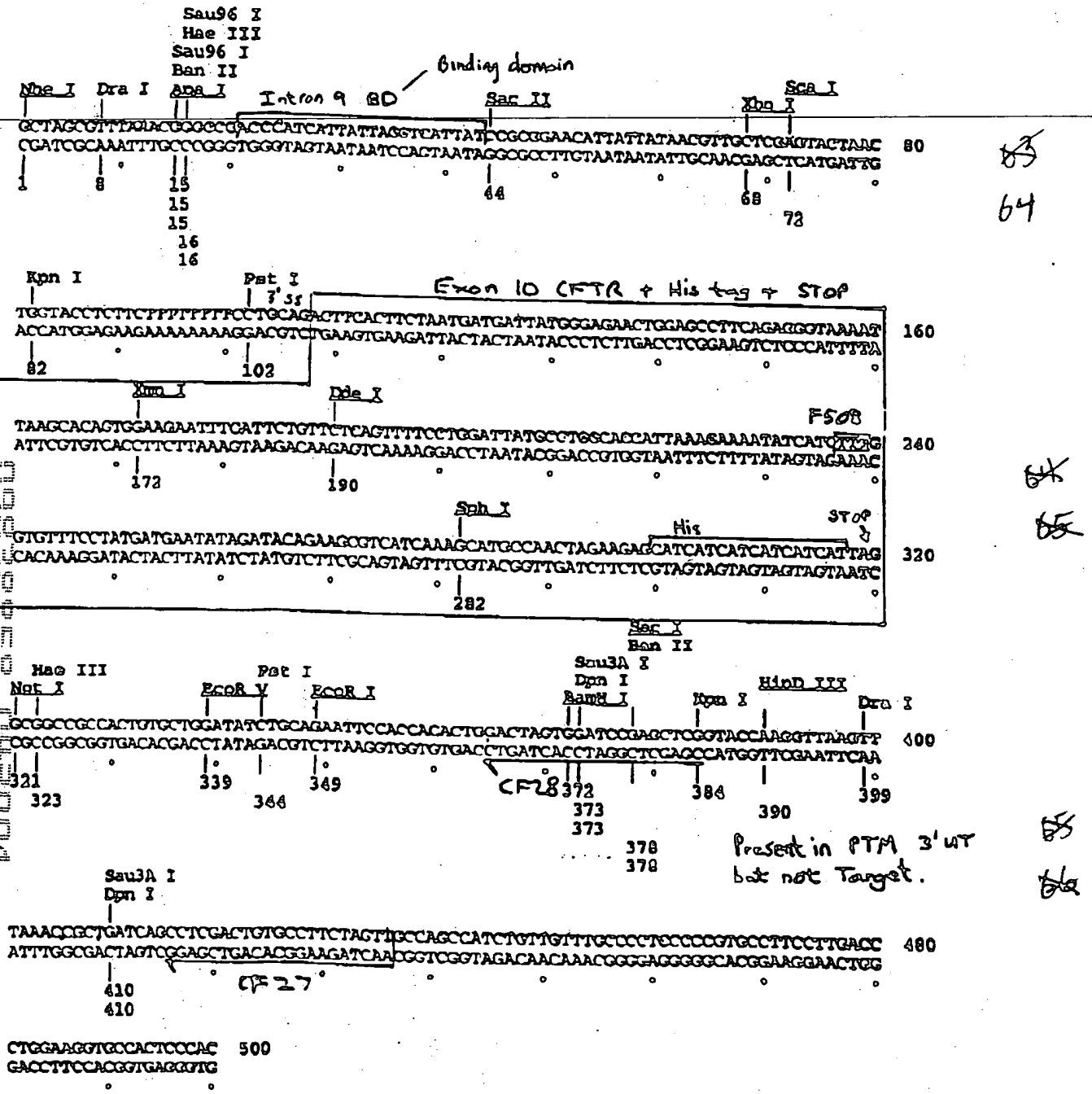
FIGURE 15

DNA sequence 500 b.p. GCTAGCGTTTAA ... TGCCACTCCCAC linear

Positions of Restriction Endonucleases ites (unique sites underlined)



Restriction Endonucleases site usage

Acc I	-	EcoR I	1	Nde I	-	Sau96 I	2
Apa I	1	EcoR V	1	Nhe I	1	Sca I	1
ApaL I	-	Hae II	-	Not I	1	Sma I	-
Avr II	-	Hae III	2	PflM I	-	Sph I	1
BamH I	1	HinC II	-	Pst I	2	Spl I	-
Ban II	2	HinD III	1	Pvu I	-	Sap I	-
Bbe I	-	Hinf I	-	Pvu II	-	Stu I	

31304-A-B
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EXPERIMENT # 2

Repair of an exogenously supplied CFTR target molecule carrying an F508 deletion in exon 10.

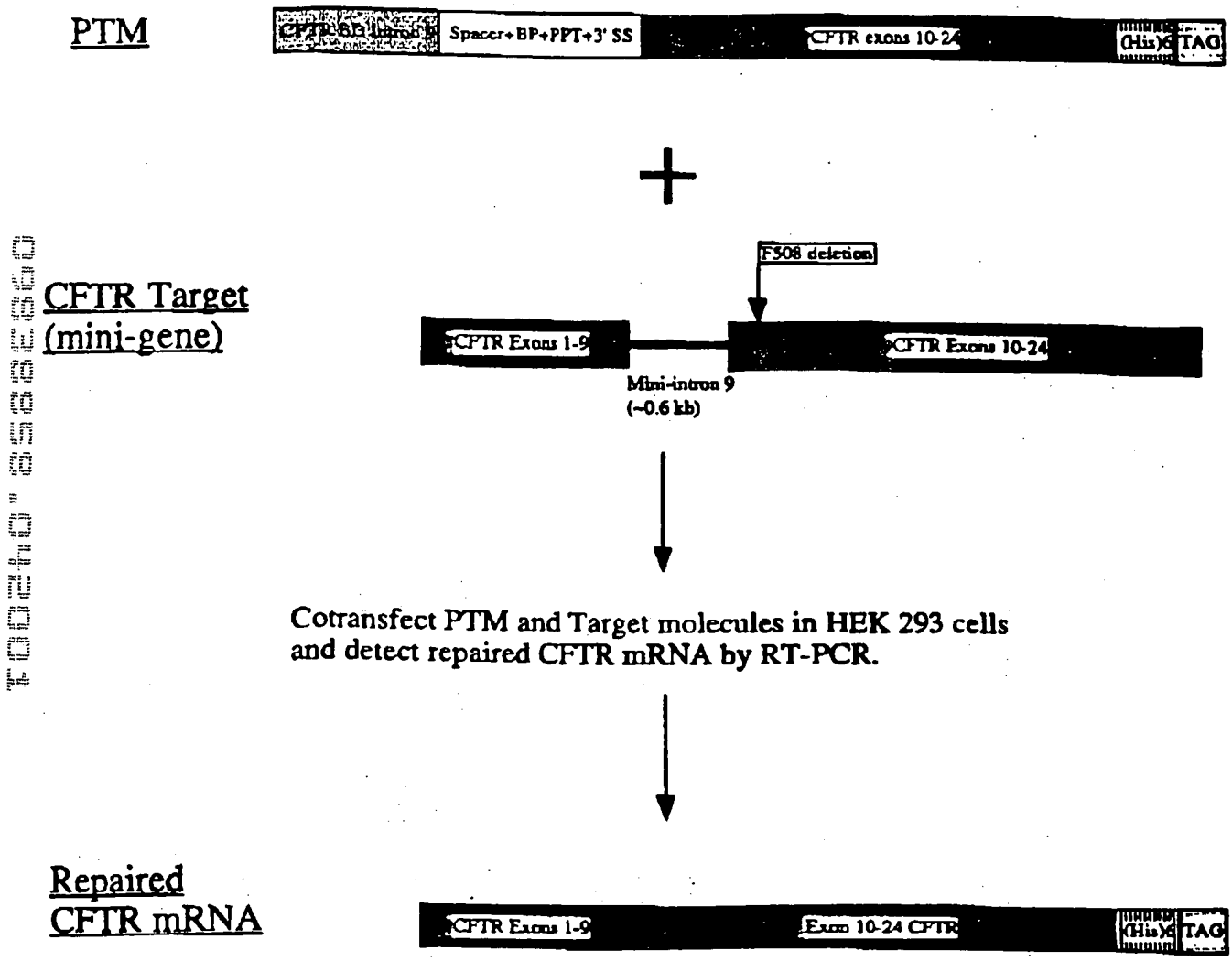

Figure 1b

31304-A-B

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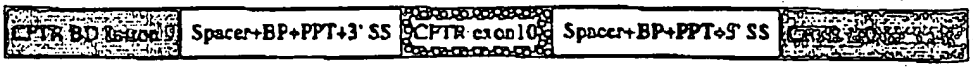
EXPERIMENT 3

Repair of endogenous CFTR transcripts by exon 10 invasion using a double splicing PTM

Double Splicing PTM



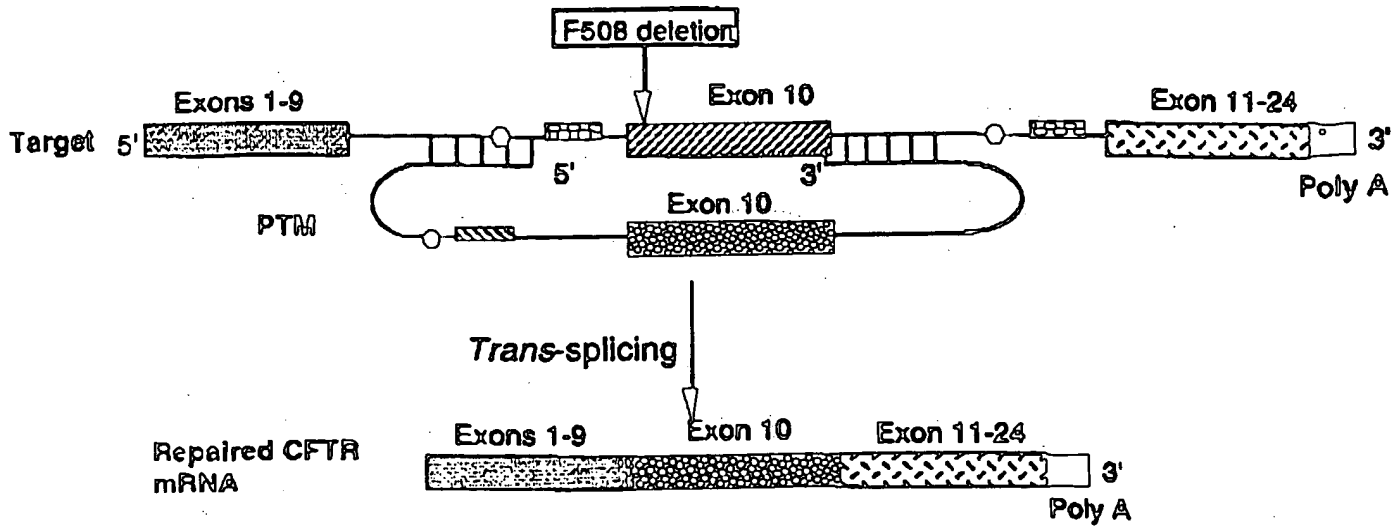


Figure 17

31304 B-A

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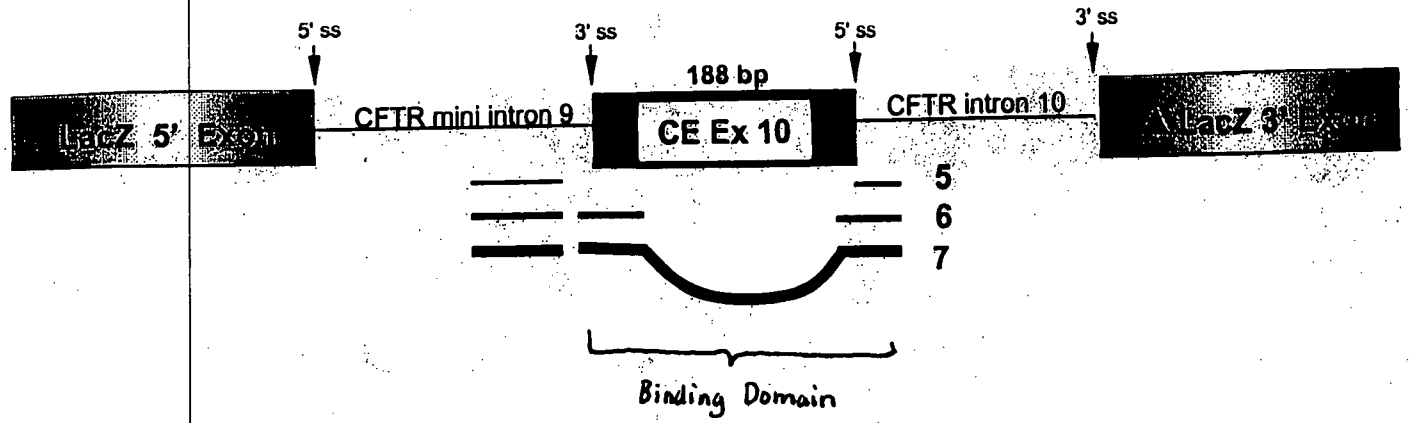
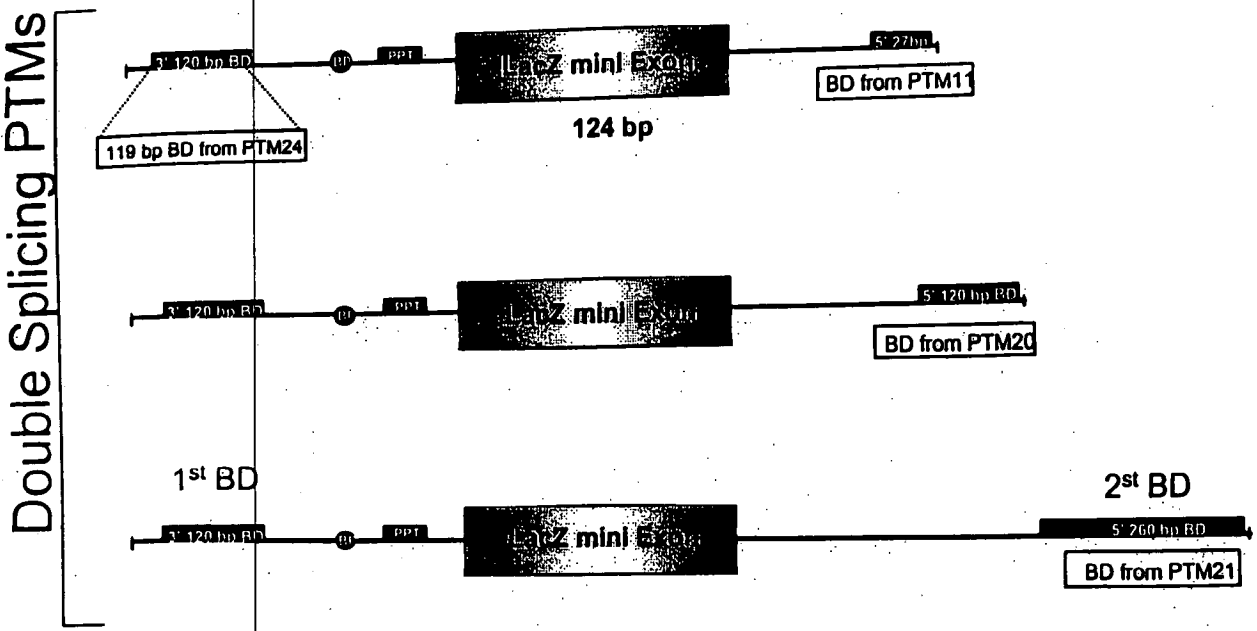
Double *Trans*-splicing Specific Target



Target DSCFT1-6

Figure 18

Double *Trans*-splicing PTMs



DSPTM-5

PTM with 27 bp BD & masks 5' single splice site

DSPTM-6

PTM with 120 bp BD & masks both 5' & 3' splice sites

DSPTM-7

PTM with 260 bp BD masking both the ss & the entire CFTR Ex10

Figure 19

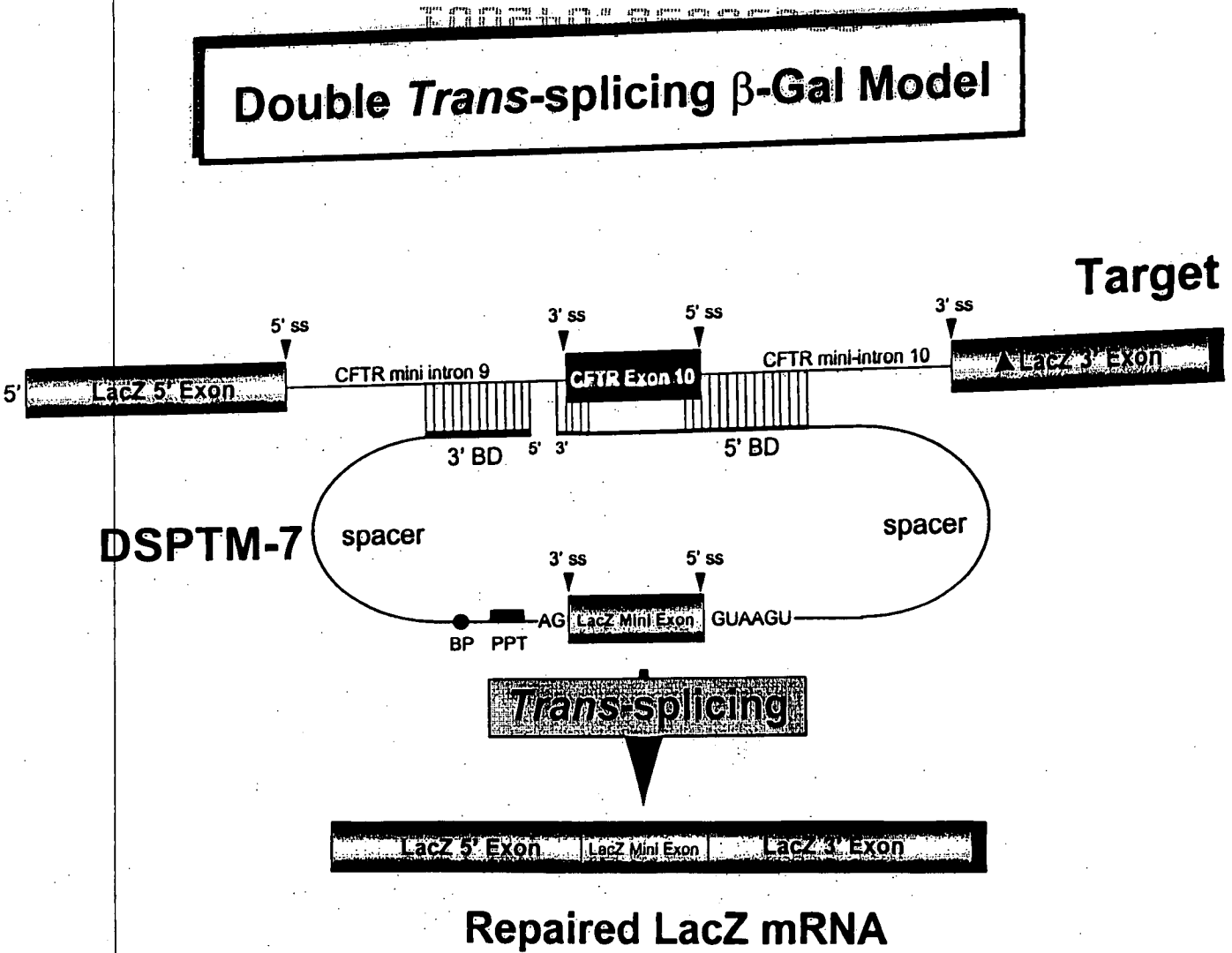
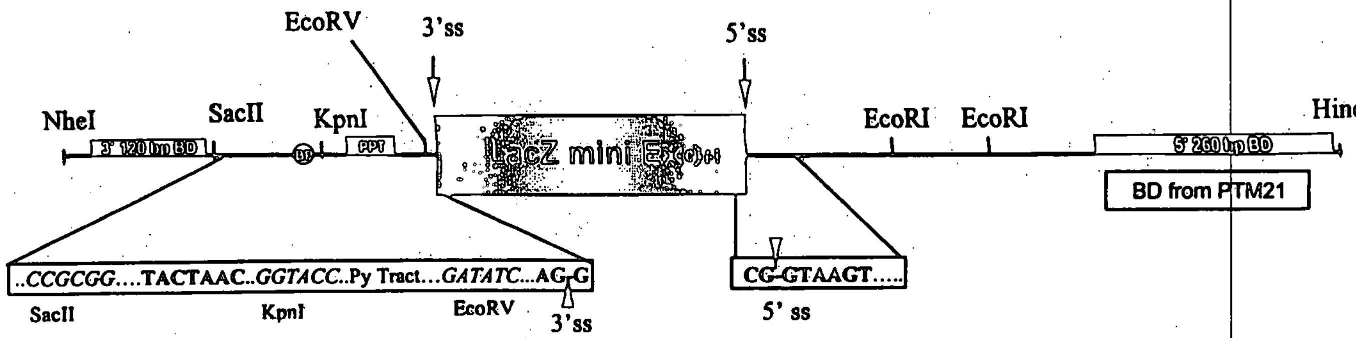

Double Trans-splicing β-Gal Model
Target
5' ss
3' ss
5' ss
3' ss
5'
LacZ 5' Exon
CFTR mini intron 9
CFTR Exon 10
CFTR mini-intron 10
LacZ 3' Exon
3' BD
5'
3'
5' BD
DSPTM-7
spacer
spacer
3' ss
5' ss
AG
LacZ Mini Exon
GUAAGU
BP
PPT
Trans-splicing
LacZ 5' Exon
LacZ Mini Exon
LacZ 3' Exon
Repaired LacZ mRNA

Figure 20

Important Structural Elements of DSPTM-7: (Double splicing PTM with all the necessary splice elements i.e. has both 3' and 5' functional splice sites and the binding domains)



(1) 3' BD (120 BP) : GATTCACTTGCTCCAATTATCATCCTAAGCAGAAGTGTATATTCTTATTTGTAAAGATTCTATTAACTCATTTGATTC AAAATATTTAAAATACTTCCTGTTTCATACTCTGCTATGCAC

(2) Spacer sequences (24 bp): AACATTATTATAACGTTGCTCGAA

(3) Branch point, pyrimidine tract and acceptor splice site: TACTAAC T *GGTACC* TCTTCTTTTTTTTTTT *GATATC* CTGCAG GGC GGC

(labels: BP, Kpn I, PPT, EcoRV, 3' ss, LacZ mini exon)

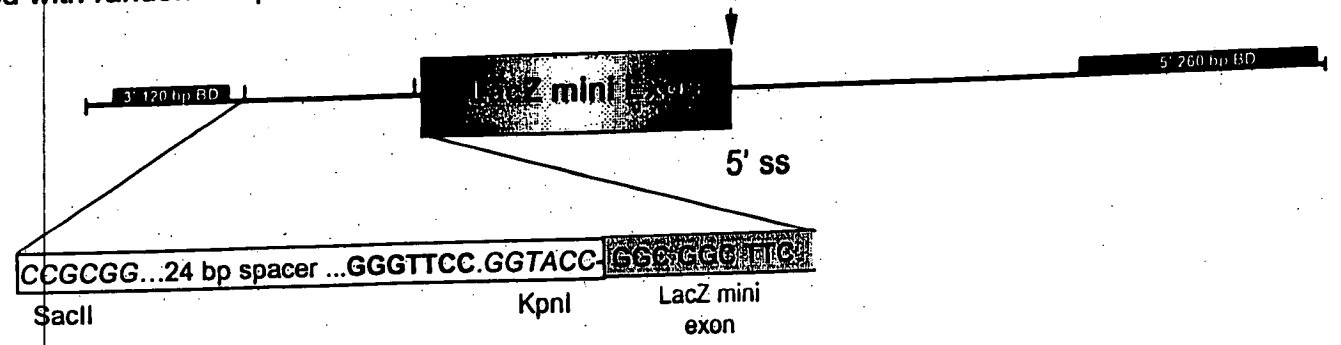
(4) 5' donor site and 2nd spacer sequence: TCA ACG *GTAAGT* GTTATCACCGATATGTGTCTAACCTGATTCGGGCCTTCGATACG CTAAGATCCACCGG

(labels: LacZ mini exon, 5' ss)

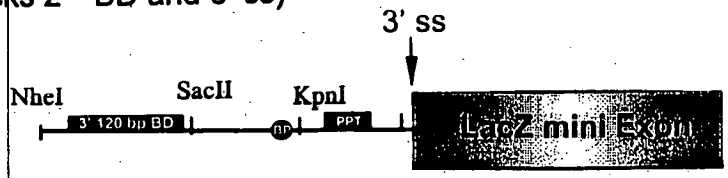
(5) 5' BD (260 BP) : TCAAAAAGTTTTCACATAATTTCTTACCTCTTCTT*GAATTC*ATGCTTTGATGACGCTTCTGTATCTATATTCATCATTGGAA ACACCAATGATTTTTCTTTAATGGTGCCTGGCATAATCCTGGAAAACTGATAACACAATGAAATTCTTCCACTGTGCTTAA AAAAACCCTCT*GAATTC*TCCATTTCTCCCATAATCATCATTACAACTGAACTCTGGAAATAAAACCCATCATTATTAACTCA TTATCAAATCACGC

Figure 21

DSPTM8 :(▲ 3' ss: 3' splice elements i.e. BP, PPT & AG dinucleotide has been deleted and replaced with random sequences, but still has the functional 5' splice site)



PTM29 (lacks 2nd BD and 5' ss)



PTM30 (lacks 1st BD and 3' ss)

Mutants

Figure 22

Accuracy of Double *Trans*-splicing Reaction

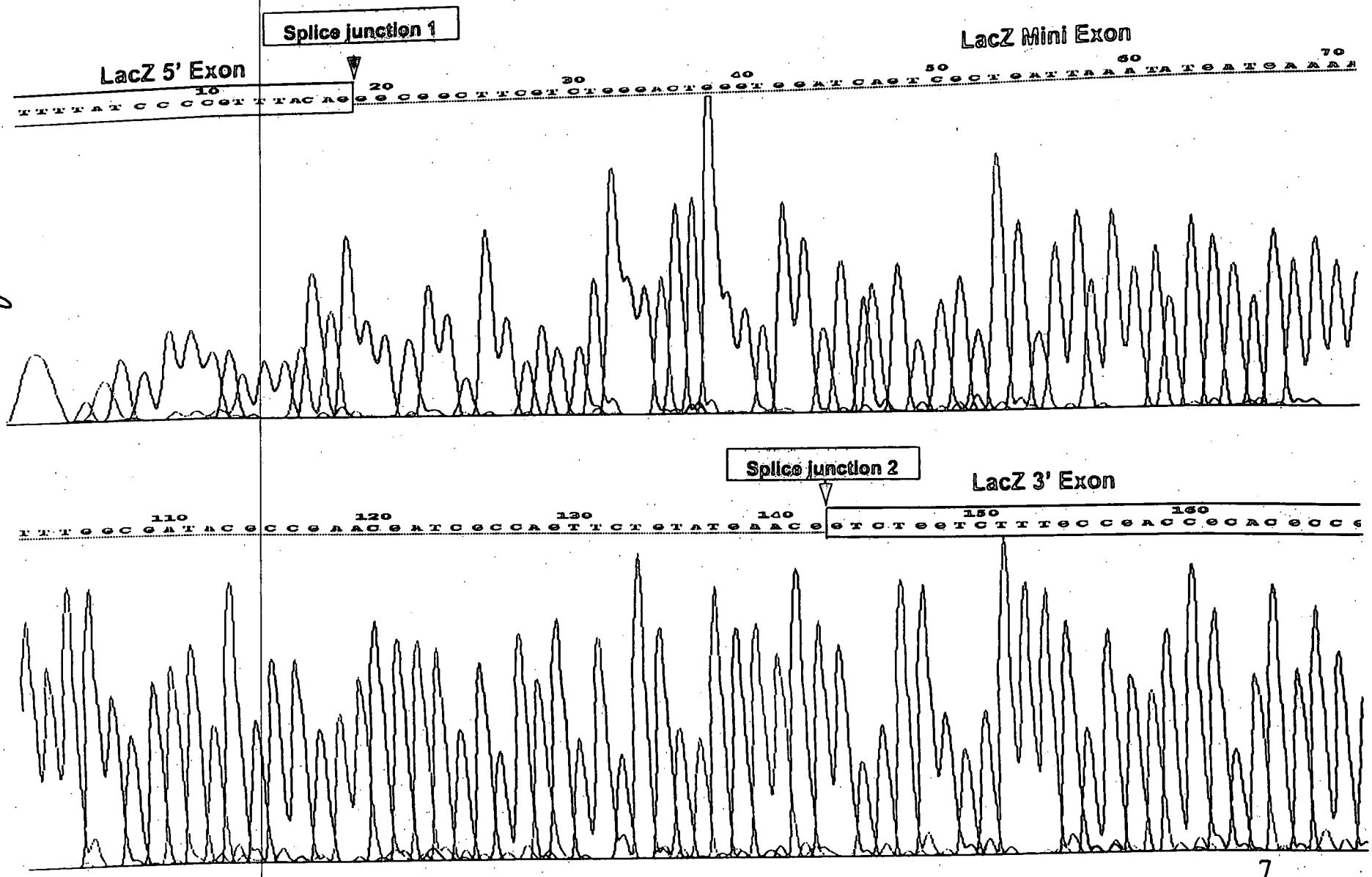
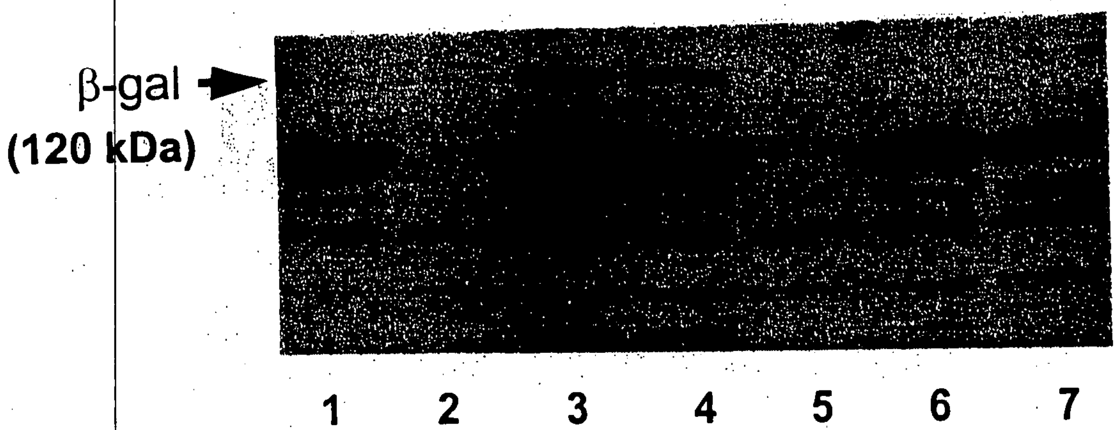


Figure 23

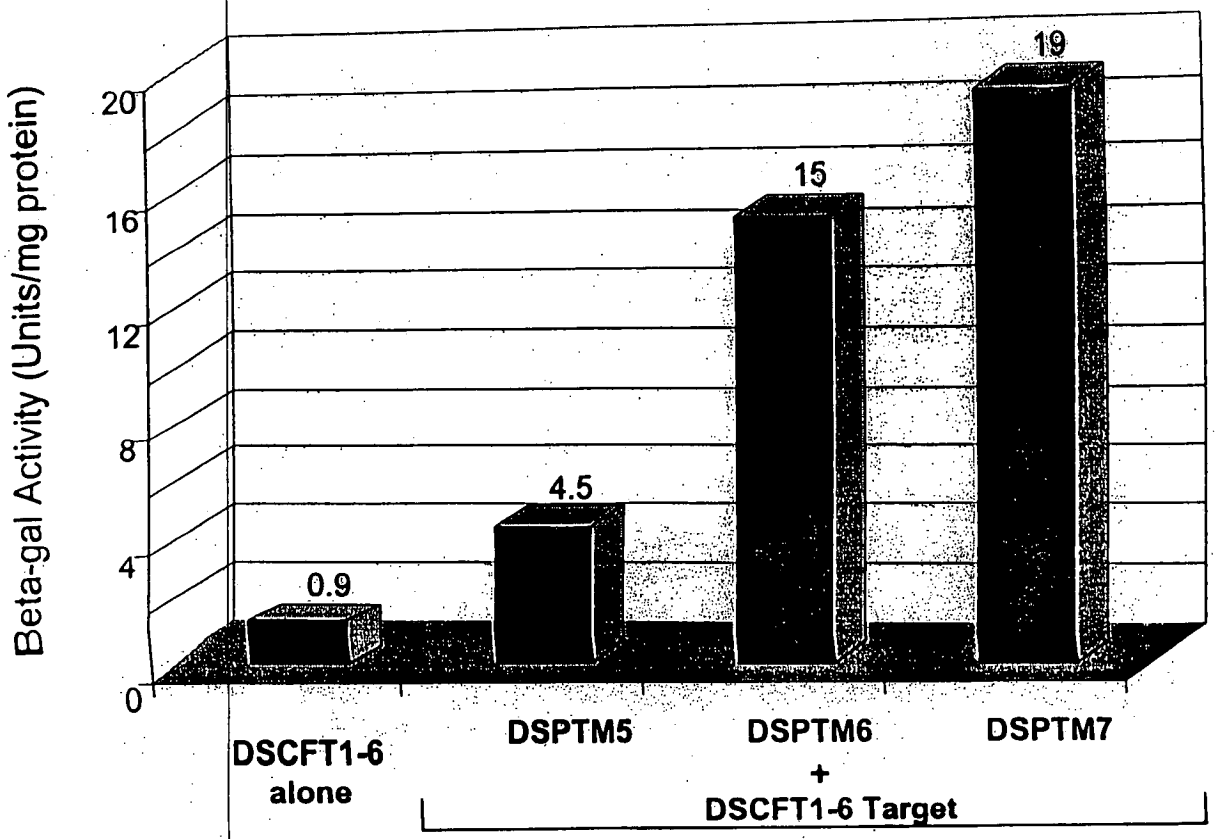
Double *Trans*-splicing Produces Full-length Protein



Lane 1: DSCFT1.6 Target alone	25 μg
Lane 2: DSPTM7	25 μg
Lane 3 Target + PTM #6	25 μg
Lane 4: Target + PTM #9	25 μg
Lane 5: Delta 3' splice mutant alone	25 μg
Lane 6: Target + Delta 3' ss	25 μg
Lane 7: Target+PTM29+30 (mutants)	25 μg

Figure 24

Restoration of β-Gal Function by Double *Trans*-splicing

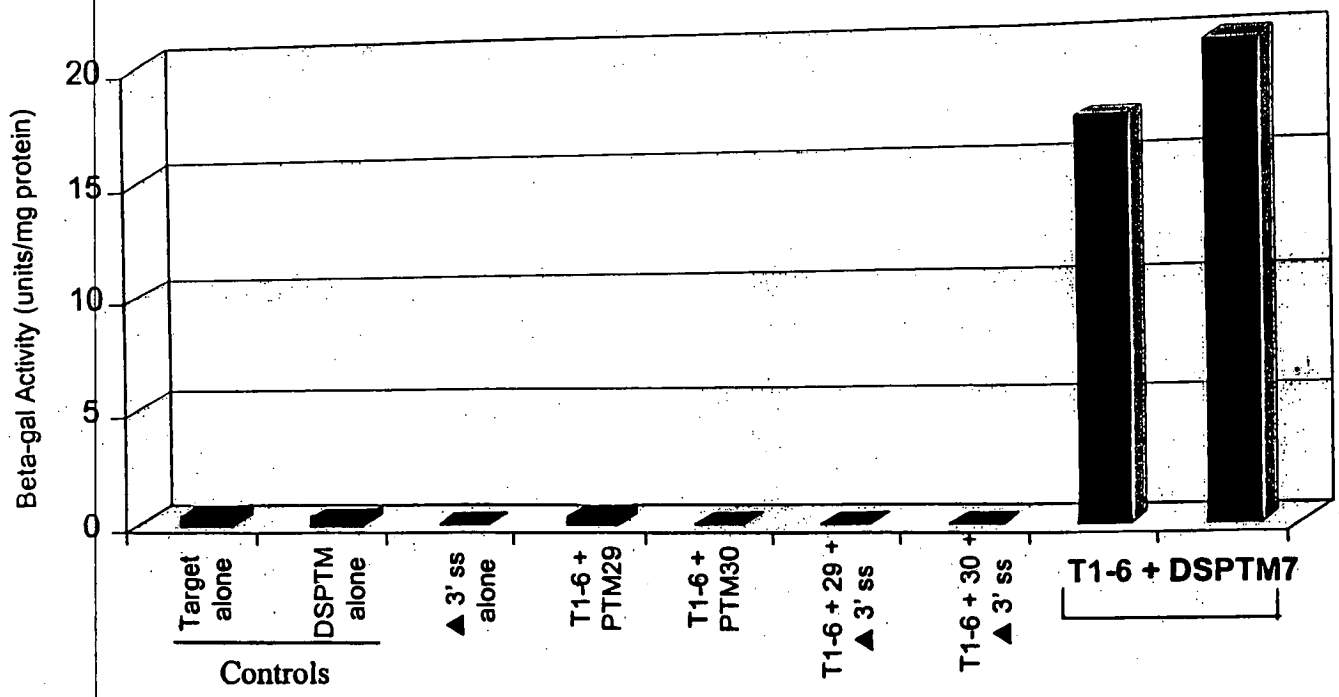


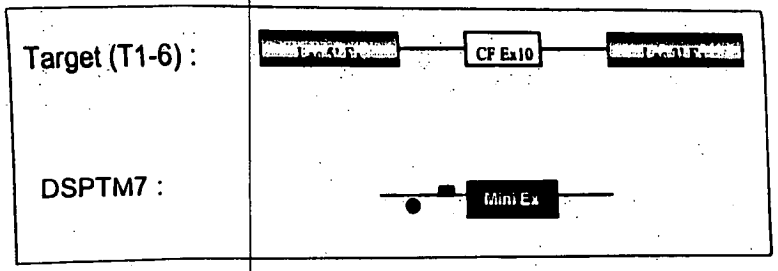
Beta-gal Activity above the Background level

DSPTM5: 5 fold
DSPTM6: 17 fold
DSPTM7: 21 fold

Figure 25

Restoration of β-gal activity is due to double RNA *trans*-splicing events





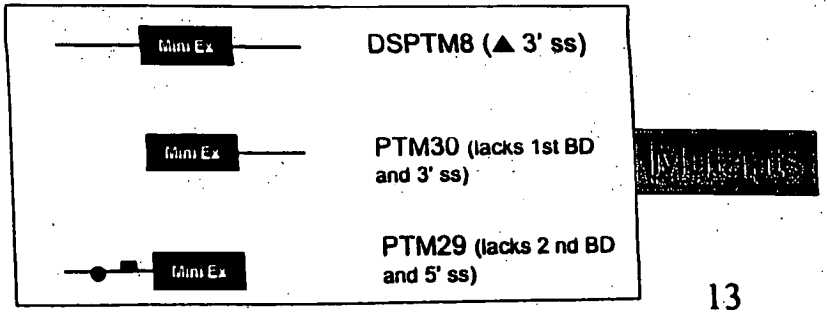
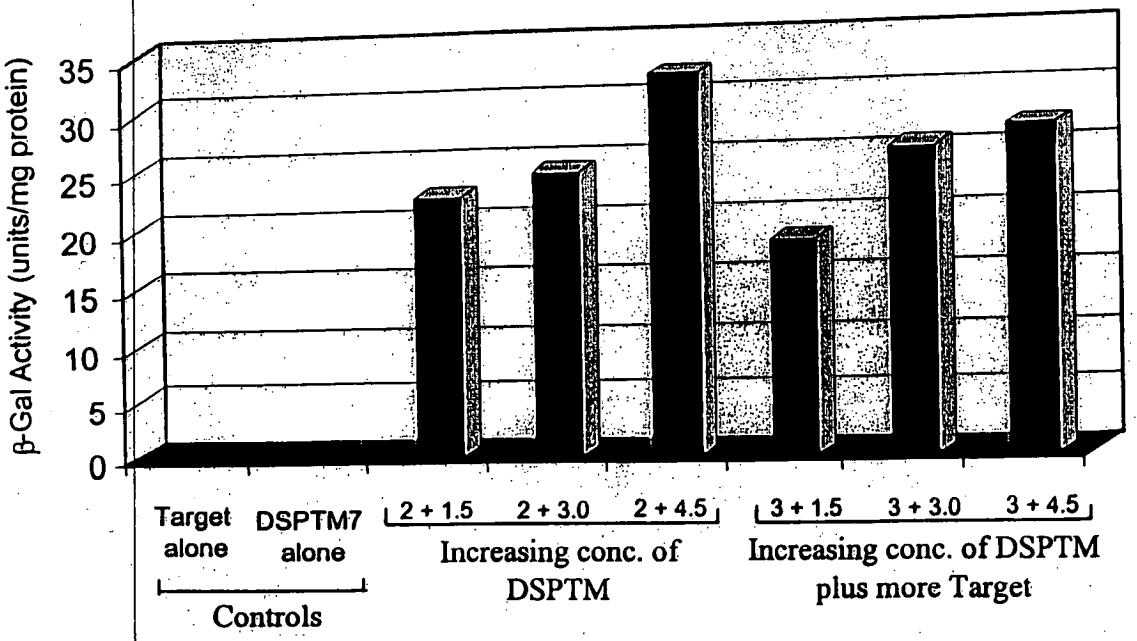


Figure 26

Double *Trans*-splicing: Titration of Target & PTM



The current level of beta-gal activity due to double *trans*-splicing is ~ 1-1.5% of the best single splice model (3' exon replacement)

Figure 27

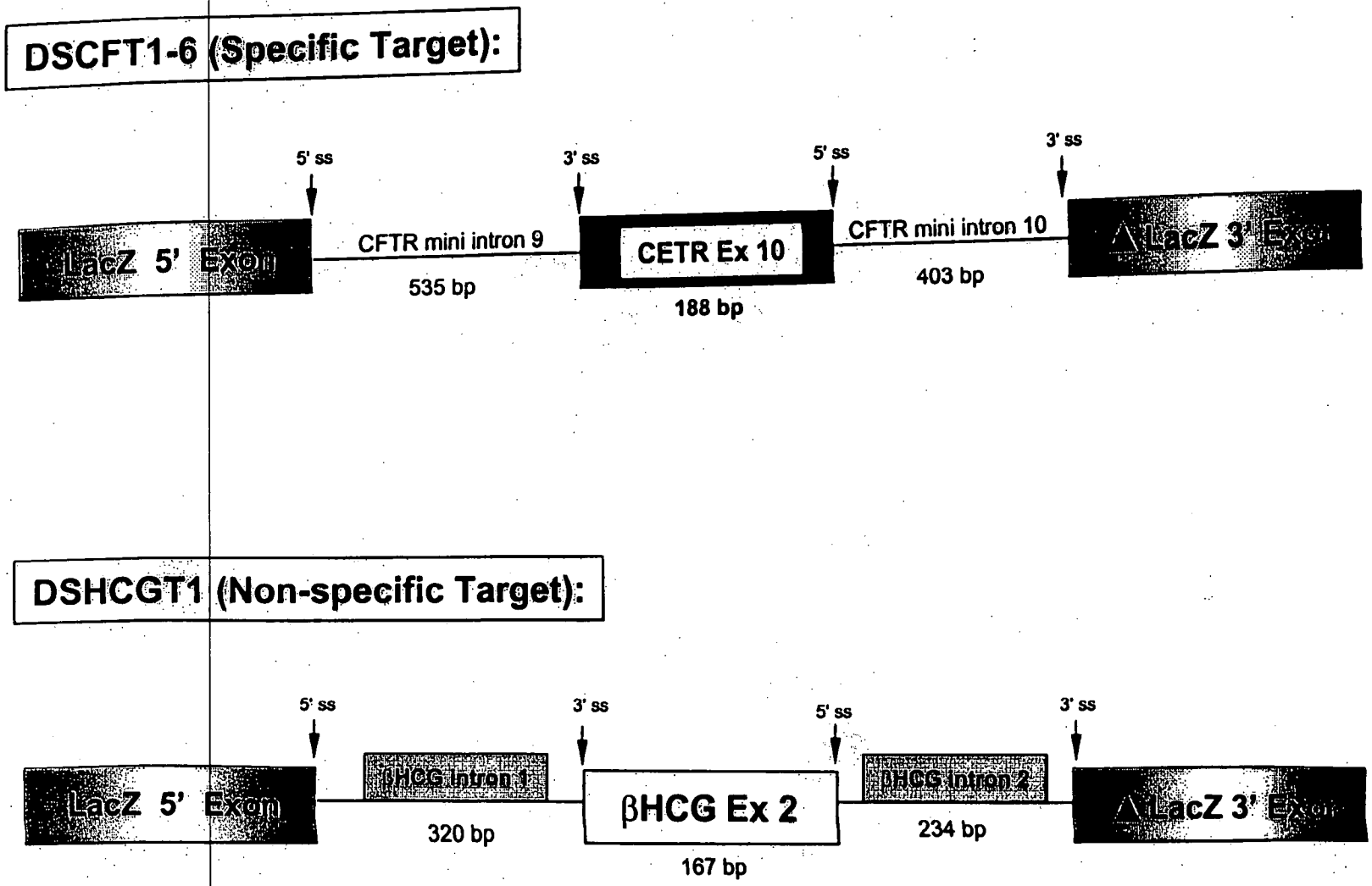

DSCFT1-6 (Specific Target):
5' ss
3' ss
5' ss
3' ss
LacZ 5' Exon
CFTR mini intron 9
535 bp
CETR Ex 10
188 bp
CFTR mini intron 10
403 bp
ΔLacZ 3' Exon
DSHCGT1 (Non-specific Target):
5' ss
3' ss
5' ss
3' ss
LacZ 5' Exon
βHCG Intron 1
320 bp
βHCG Ex 2
167 bp
βHCG Intron 2
234 bp
ΔLacZ 3' Exon

Figure 28

Specificity of double *trans*-splicing Reaction

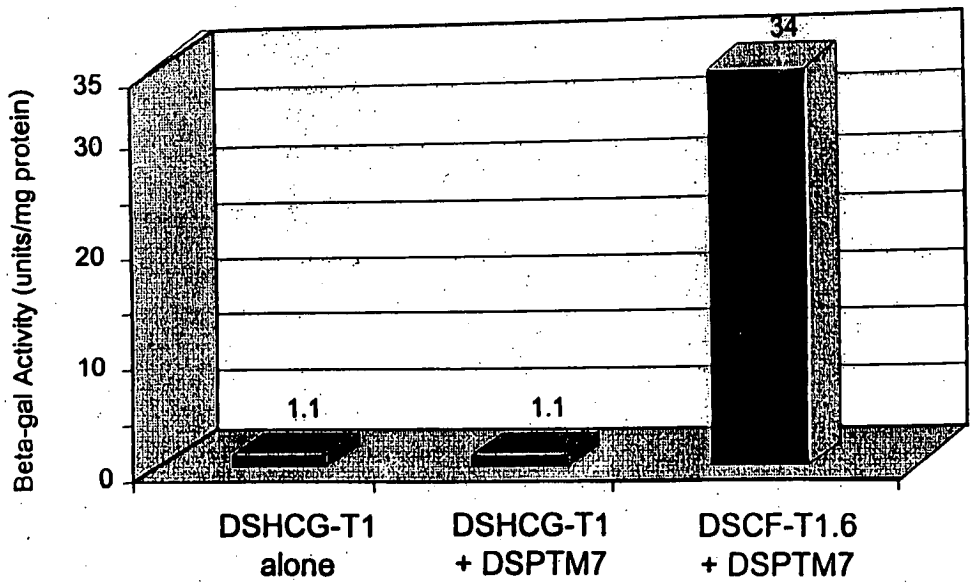


Figure 29

Replacement of a Single Internal Exon

Schematic diagram of a PTM binding to a CFTR ΔF508 target

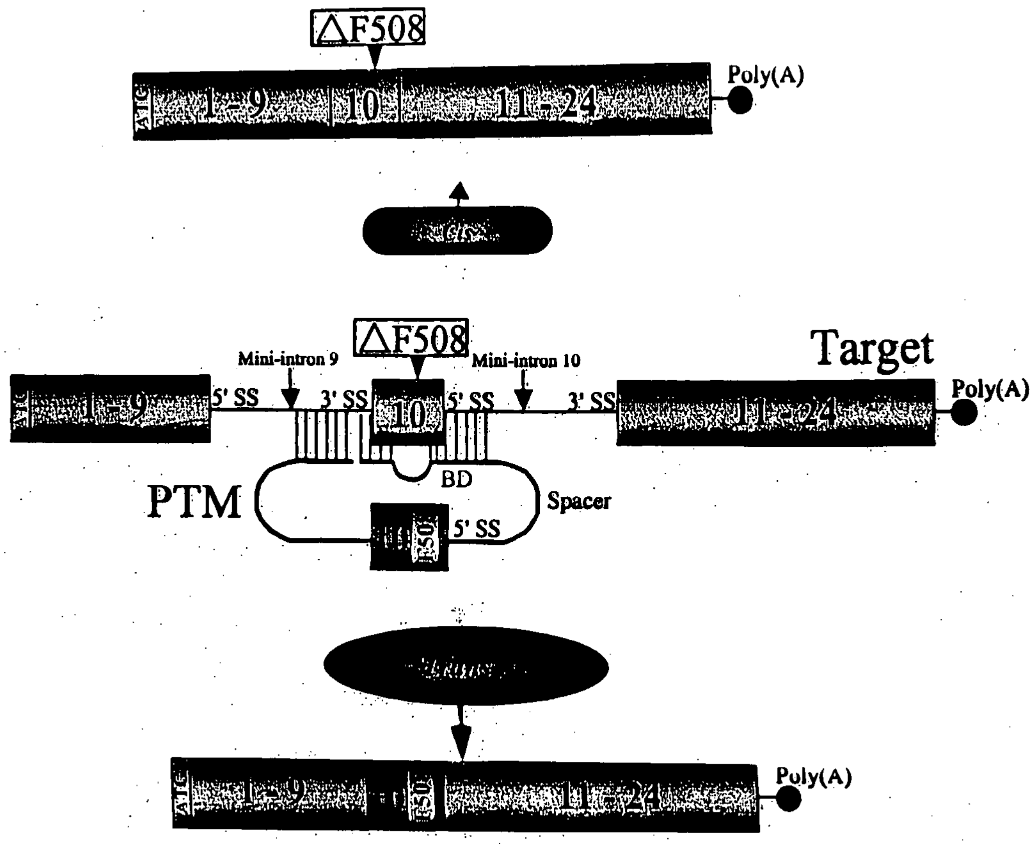
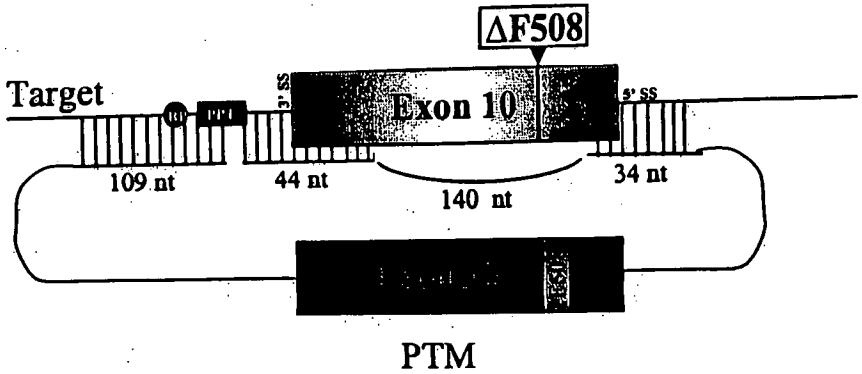


Figure 30

INTRONN

PTM with a long binding domain masking two splice sites and part of exon 10 in a mini-gene target.



ACGAGCTTGCTCATGATGATCATGGGCGAGTTAGAACCAAGTGAAGGCAAGATCAAACATTCCG
GCCGCATCAGCTTTTGCAGCCAATTCAGTTGGATCATGCCCGGTACCATCAAGGAGAACATAAT
CTTCGGCGTCAGTTACGACGAGTACCGCTATCGCTCGGTGATTAAGGCCTGTCAGTTGGAGGAG

MCU in exon 10 of PTM

88 of 192 (46%) bases in PTM exon 10 are not complementary to its binding domain (bold and underlined).

Figure 31

INTRONN

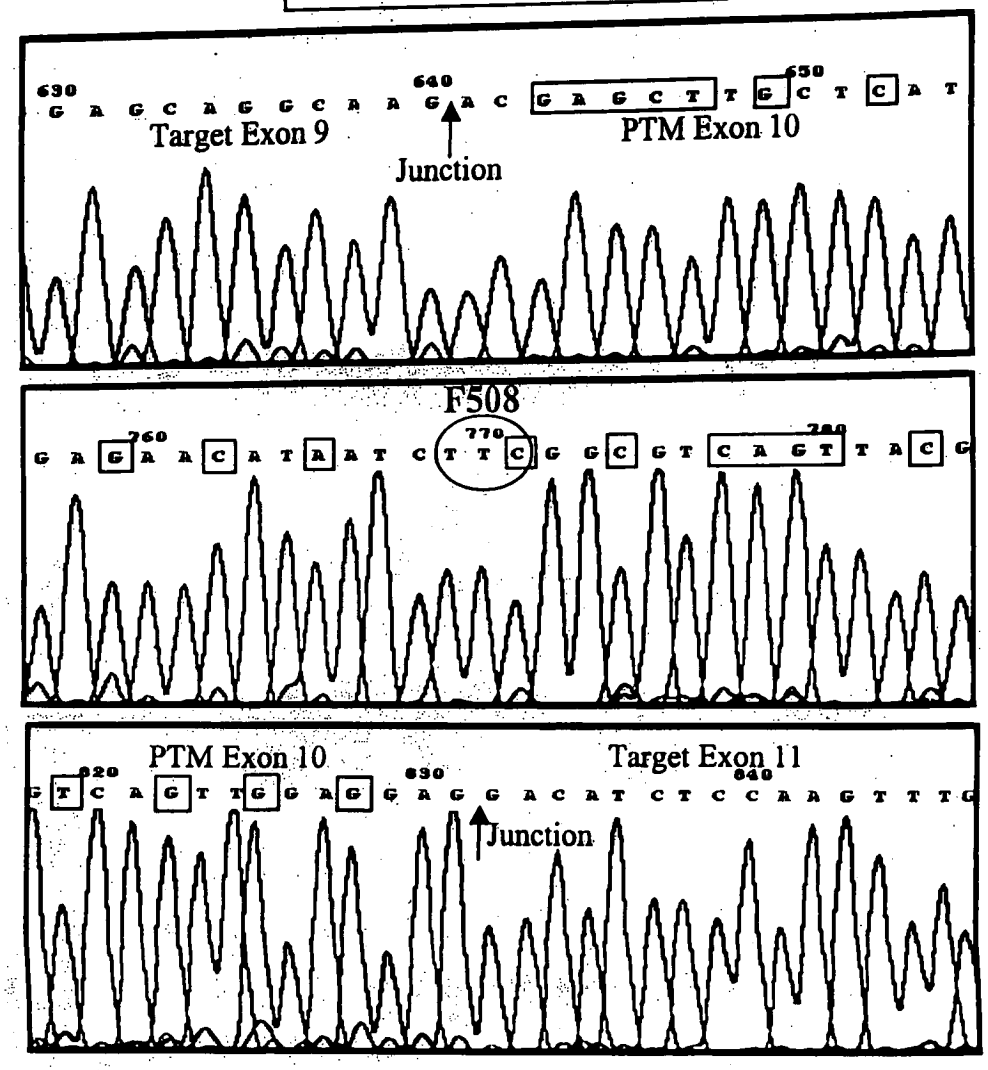

Sequence of a double *trans*-spliced product
Target Exon 9
Junction
PTM Exon 10
F508
PTM Exon 10
Target Exon 11
Junction
□ = MCU in PTM exon 10

Figure 32

CFTR Repair: 5' Exon Replacement

Schematic diagram of a PTM binding to the splice site of intron 10 of a mini-gene target

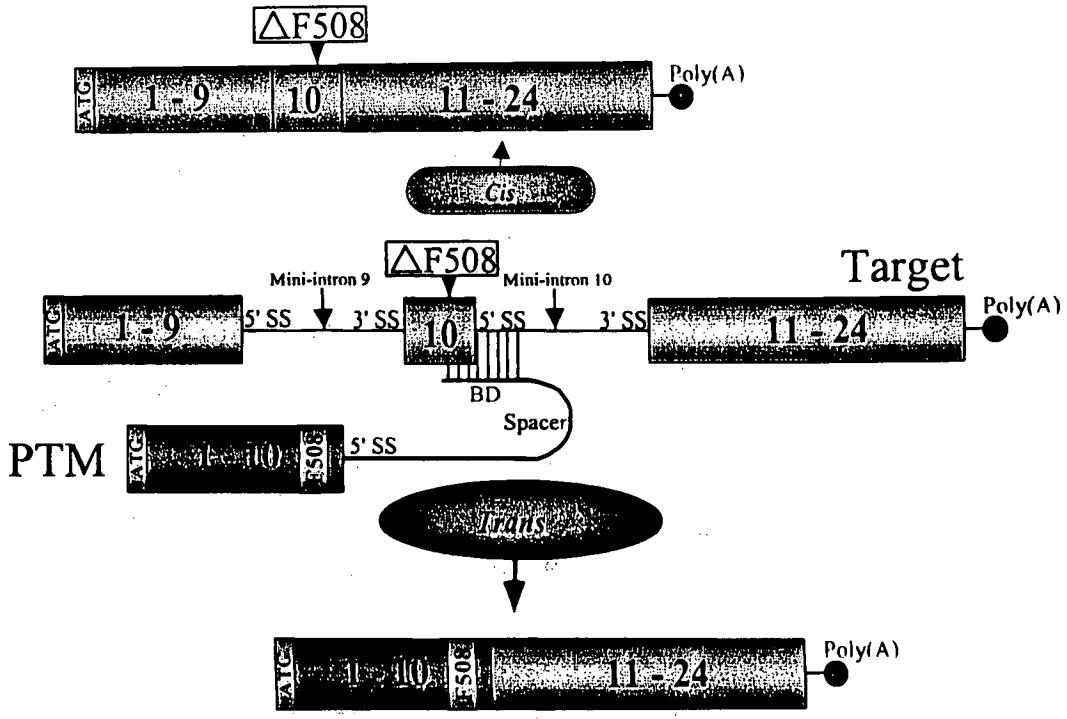
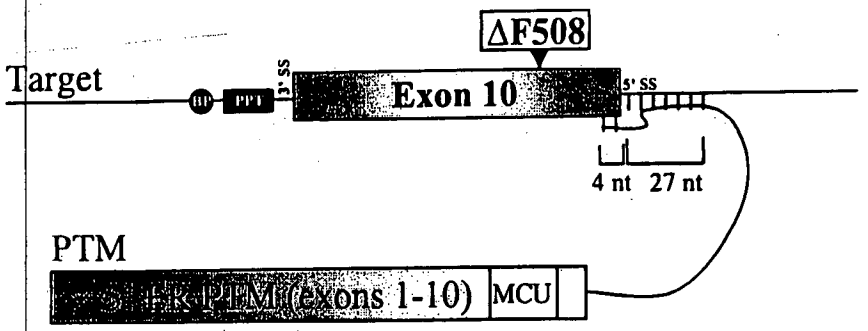
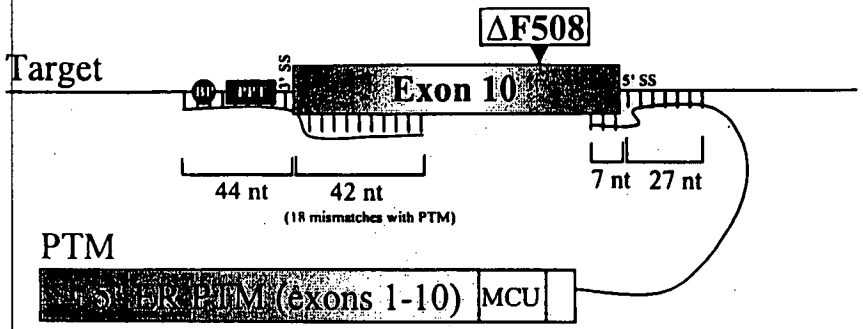


Figure 33



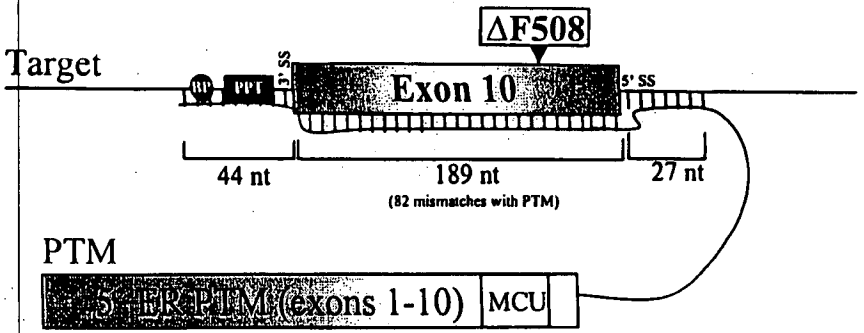
A

PTM with a short binding domain masking a single splice site in a mini-gene target.



B

PTM with a long binding domain masking two splice sites in a mini-gene target.

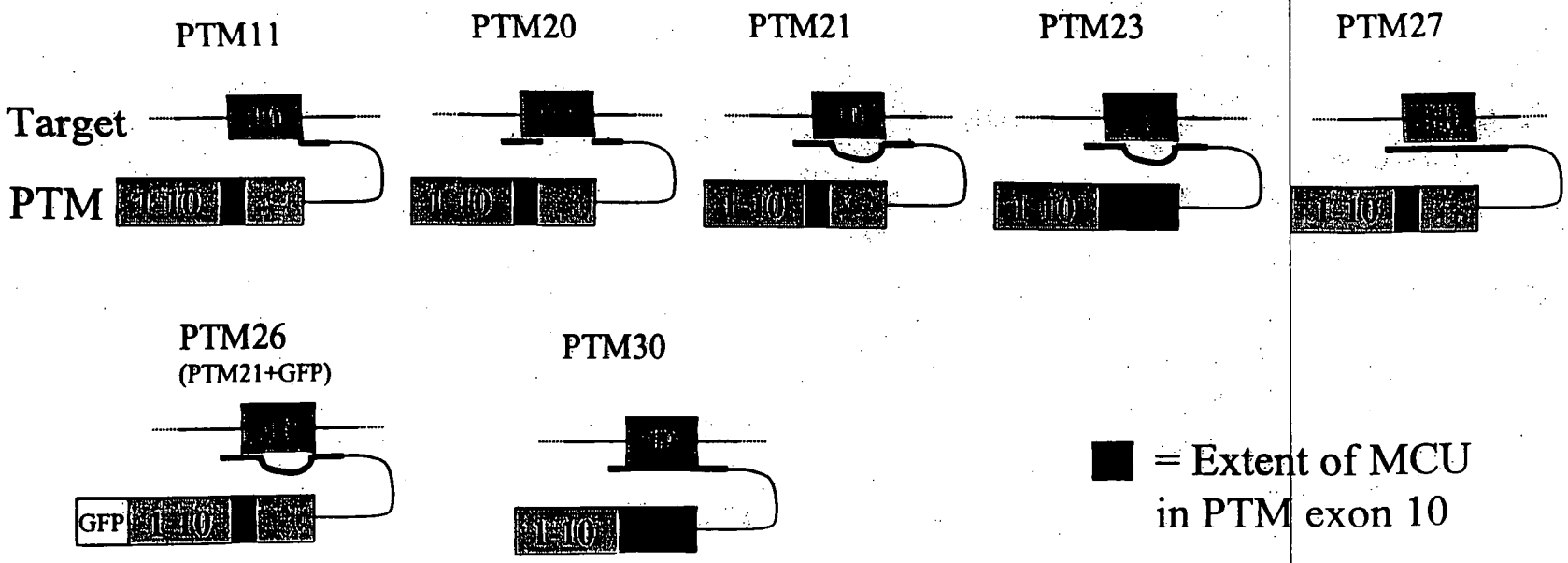


C

PTM with a long binding domain masking two splice sites and the whole of exon 10 in a mini-gene target.

Figure 34

Sheet 41 of 66

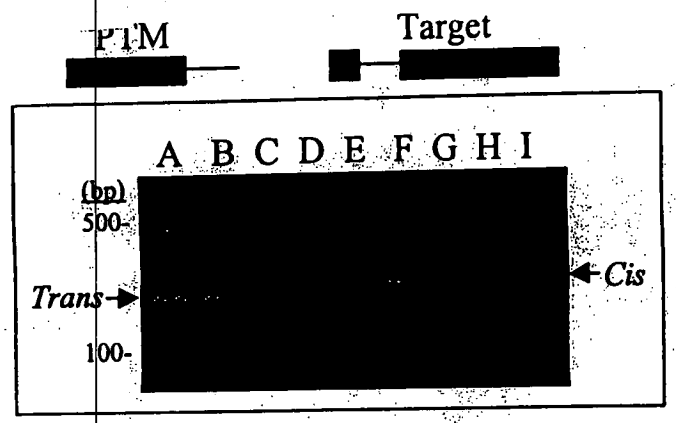


MCU in exon 10 of PTM

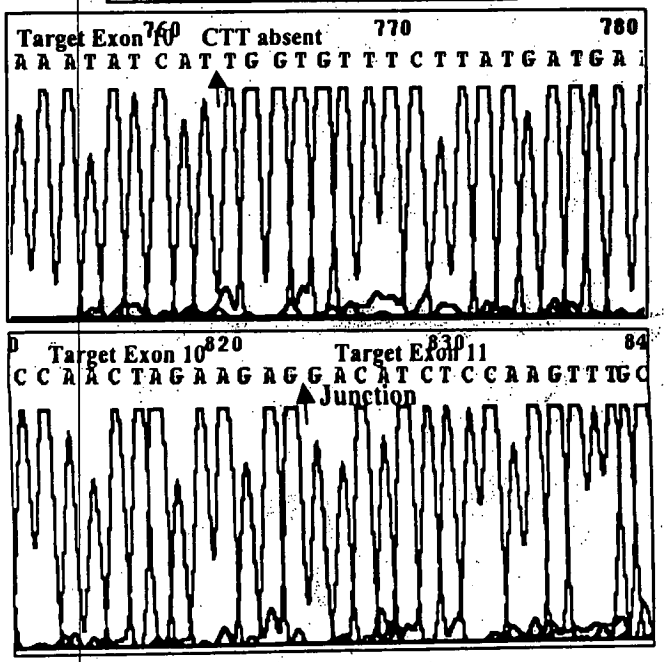
88 of 192 (46%) bases in PTM exon 10 are not complementary to its binding domain.

ACGAGCTTGCTCATGATGATCATGGGCGAGTTAGAACCAAGTGAAGGCAAGATCAAACATTCCG
GCCGCATCAGCTTTTGCAGCCAATTCAGTTGGATCATGCCCGGTACCATCAAGGAGAACATAAT
CTTCGGCGTCAGTTACGACGAGTACCGCTATCGCTCGGTGATTAAGGCCTGTCAGTTGGAGGAG

Figure 35



A. *Cis*-spliced product
[Primers CF1 + CF111]



B. *Trans*-spliced product
[Primers CF93 + CF111]

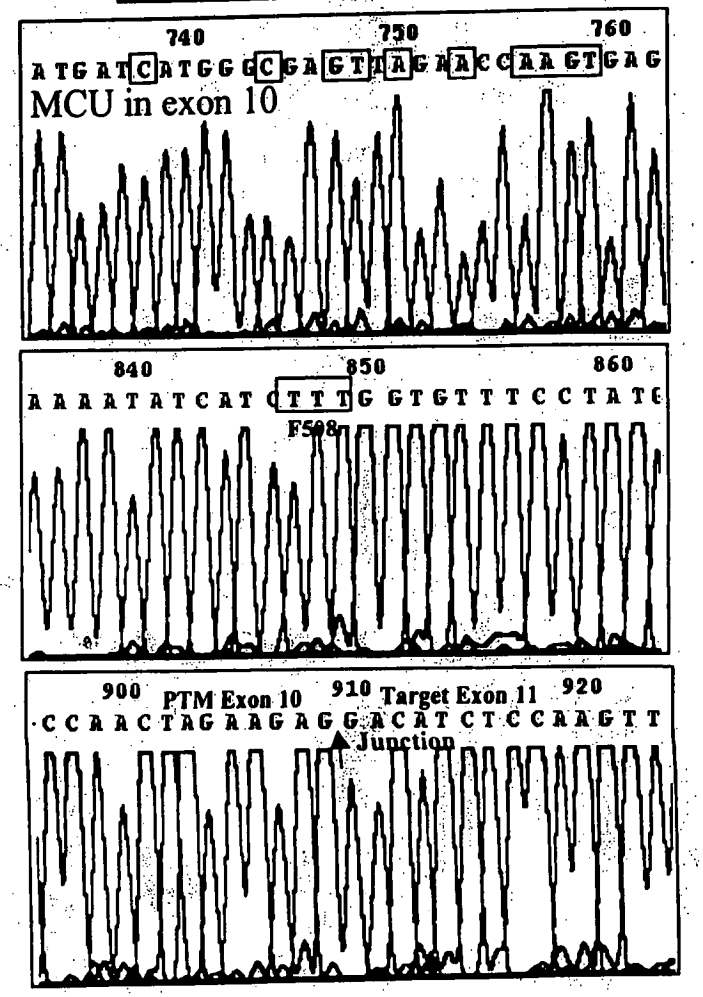


Figure 36

A

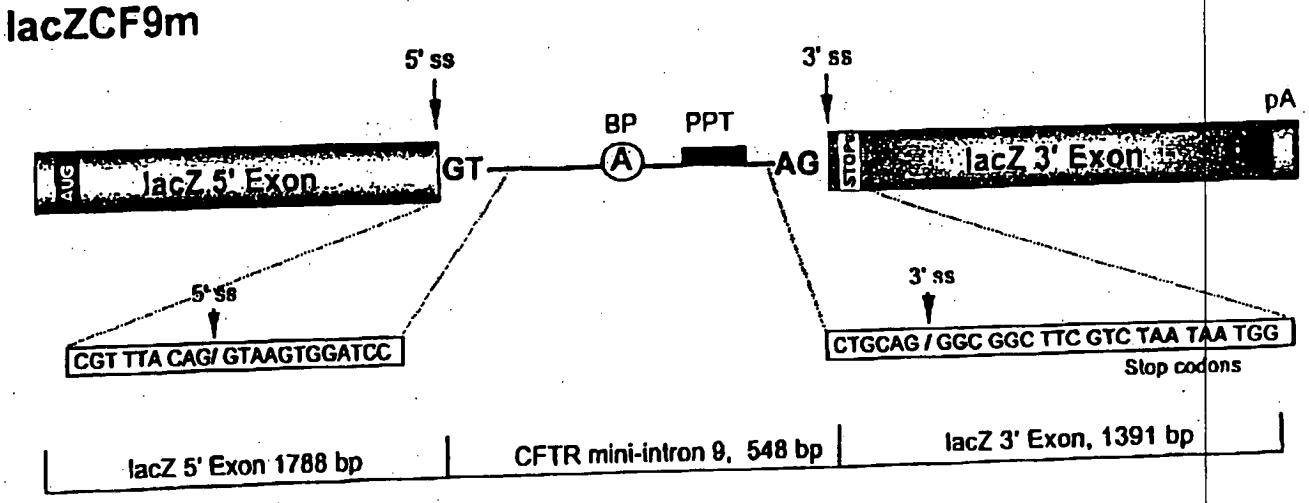


Figure 37 A

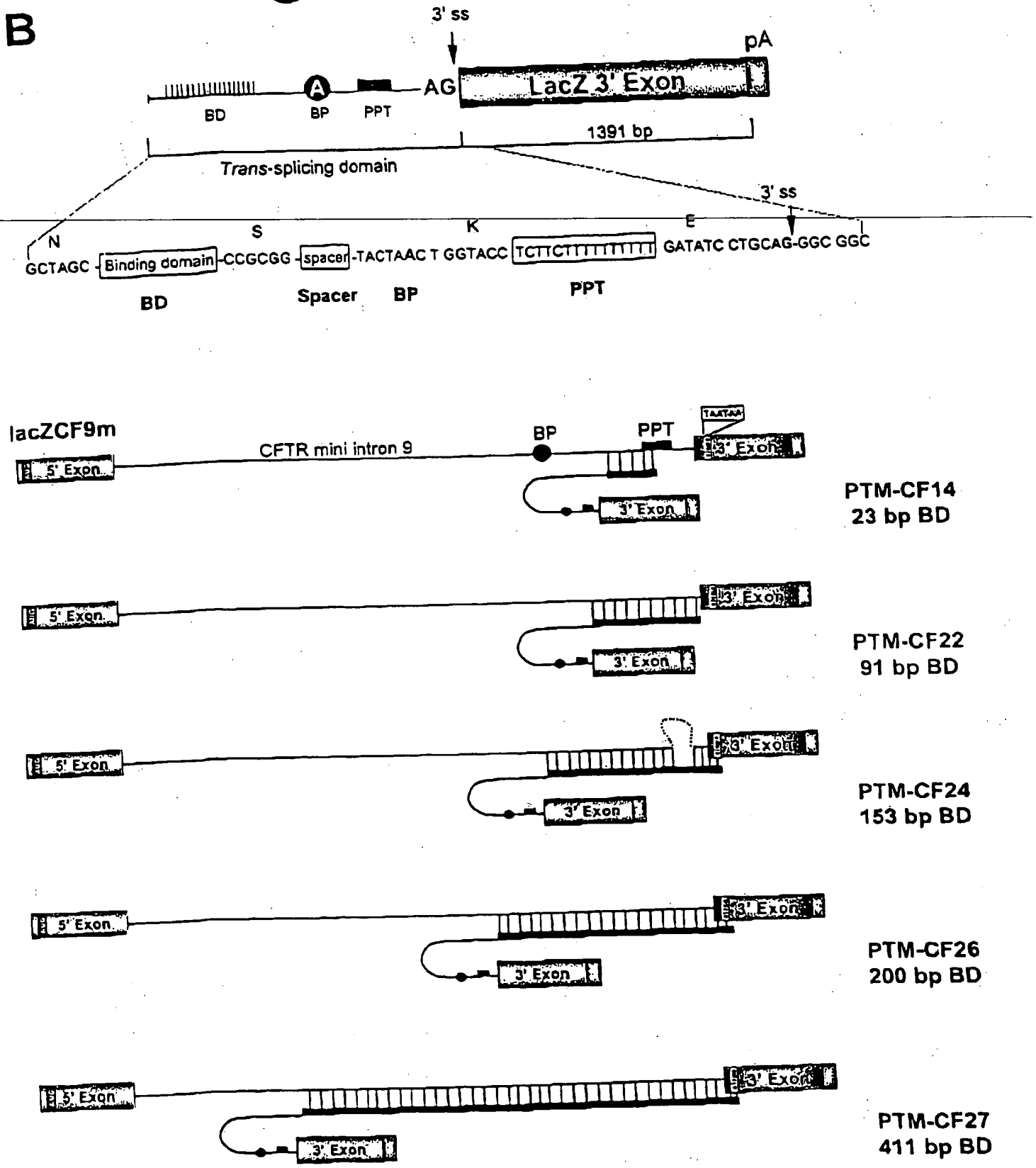

B
3' ss
pA
AG
LacZ 3' Exon
BD
BP
PPT
1391 bp
Trans-splicing domain
3' ss
N
S
K
E
GCTAGC
Binding domain
CCGCGG
spacer
TACTAAC T GGTACC
TCTTCTTTTTTTTT
GATATC CTGCAG GGC GGC
BD
Spacer
BP
PPT
lacZCF9m
CFTR mini intron 9
BP
PPT
TAATAA
5' Exon
3' Exon
PTM-CF14
23 bp BD
PTM-CF22
91 bp BD
PTM-CF24
153 bp BD
PTM-CF26
200 bp BD
PTM-CF27
411 bp BD

Figure 37B

C

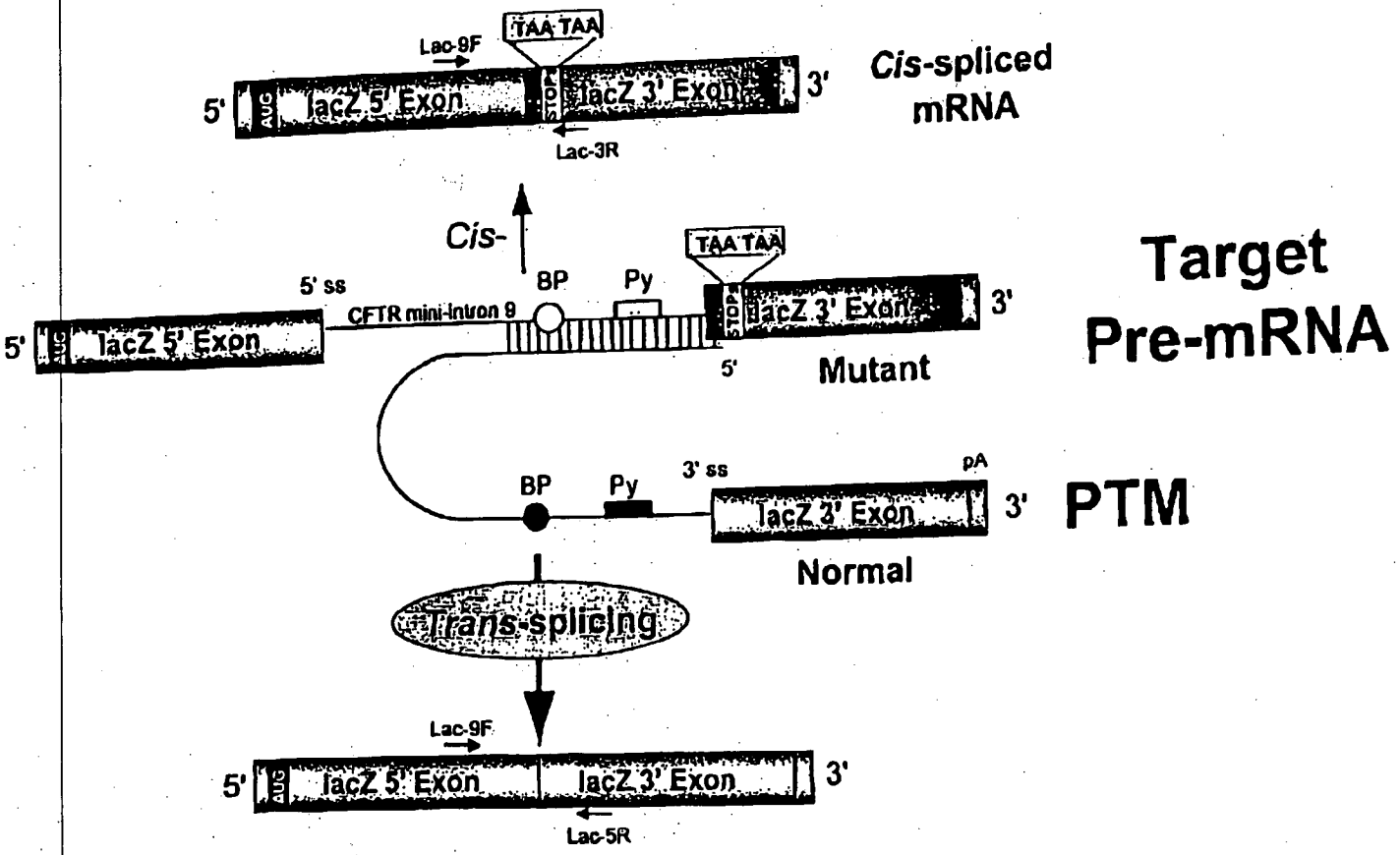

Lac-9F
TAA TAA
5'
AUG
lacZ 5' Exon
STOP
lacZ 3' Exon
3'
Lac-3R
Cis-spliced mRNA
Cis-
5' ss
BP
Py
TAA TAA
CFTR mini-intron 9
STOP
Target Pre-mRNA
Mutant
BP
Py
3' ss
pA
PTM
Normal
Trans-splicing
Lac-9F
Lac-5R
Repaired lacZ mRNA

Figure 37C

A

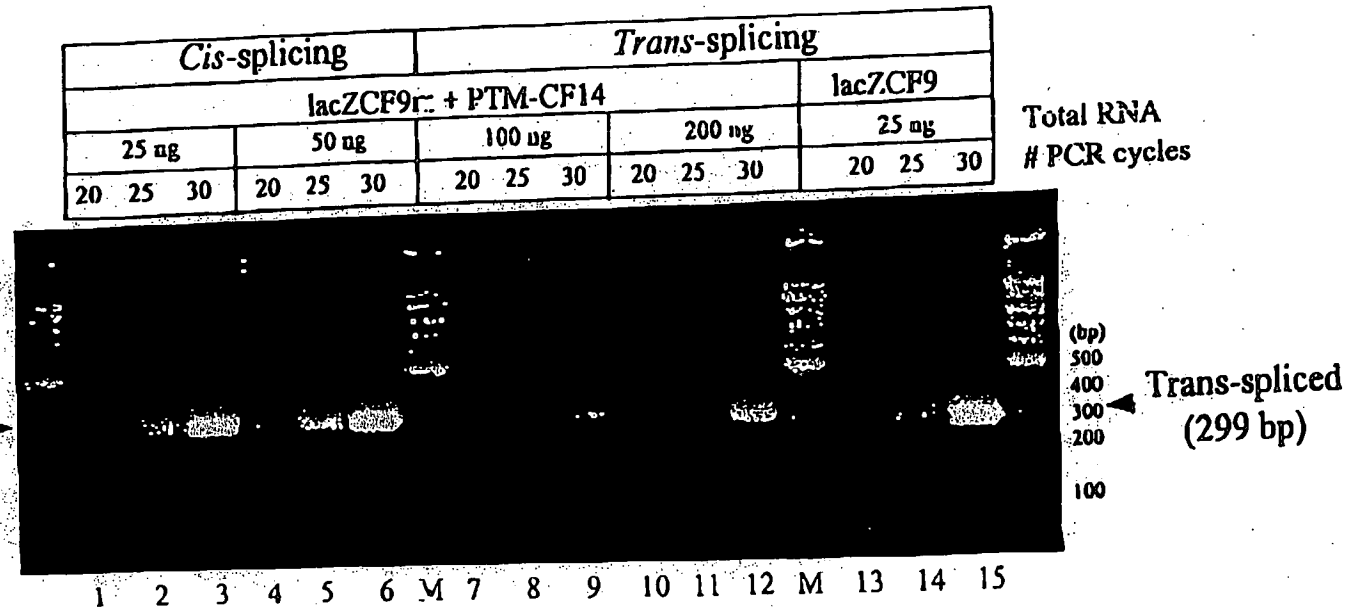
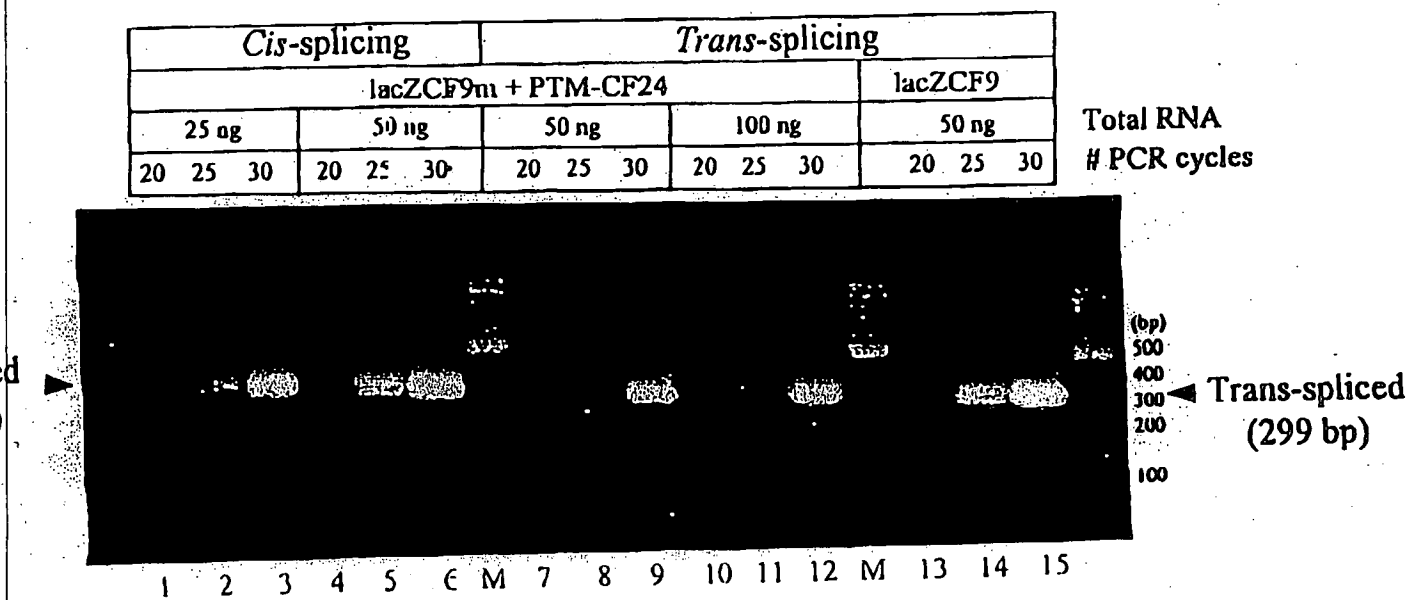

Cis-splicing
Trans-splicing
lacZCF9m + PTM-CF14
lacZCF9
25 ng
50 ng
100 ng
200 ng
25 ng
20 25 30
Total RNA
PCR cycles
Cis-spliced
(303 bp)
Trans-spliced
(299 bp)
(bp)
500
400
300
200
100
1 2 3 4 5 6 M 7 8 9 10 11 12 M 13 14 15

Figure 38 A


Cis-splicing
Trans-splicing
lacZCF9m + PTM-CF24
lacZCF9
25 ng
50 ng
50 ng
100 ng
50 ng
20 25 30
Total RNA
PCR cycles
Cis-spliced
(303 bp)
Trans-spliced
(299 bp)
(bp)
500
400
300
200
100
1 2 3 4 5 6 M 7 8 9 10 11 12 M 13 14 15

B

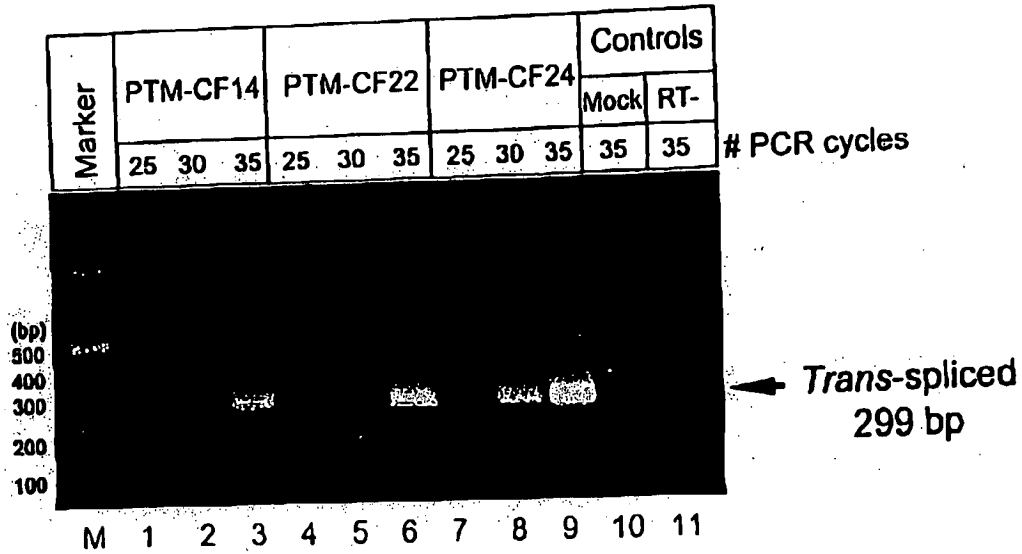


Figure 38B

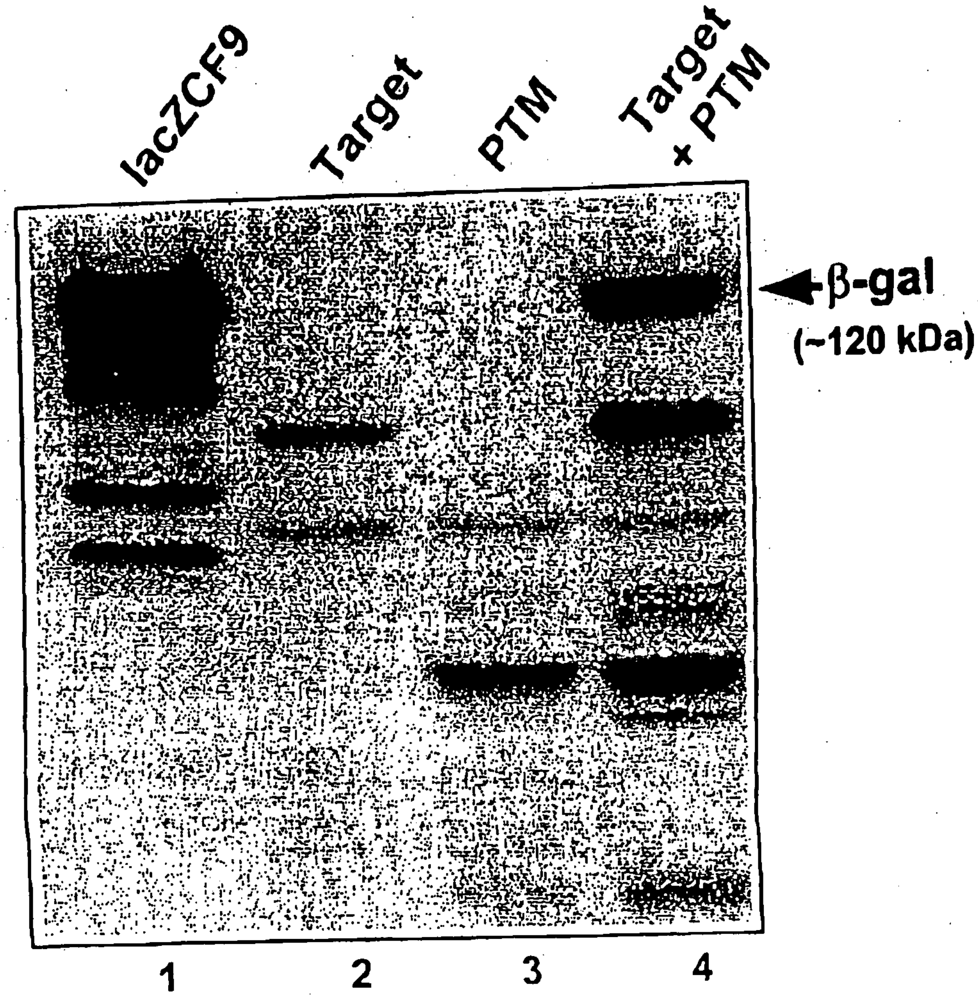


Figure 39

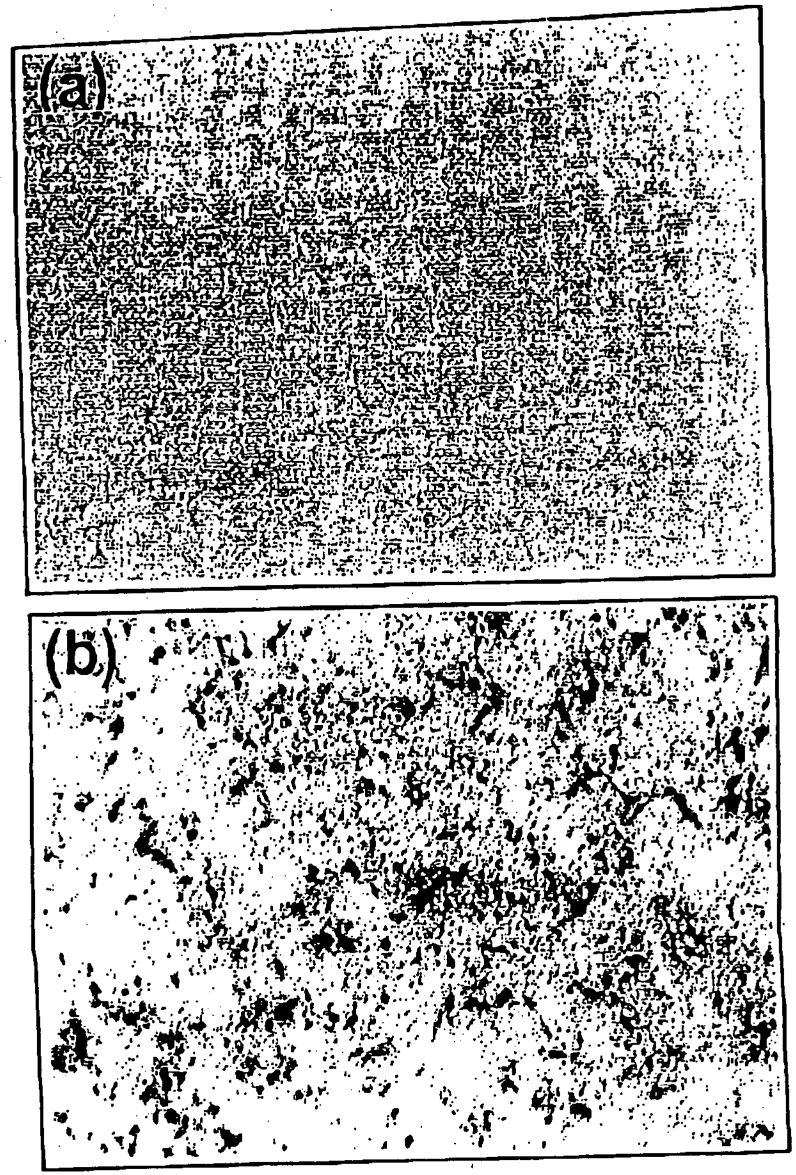


Figure 40A

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B

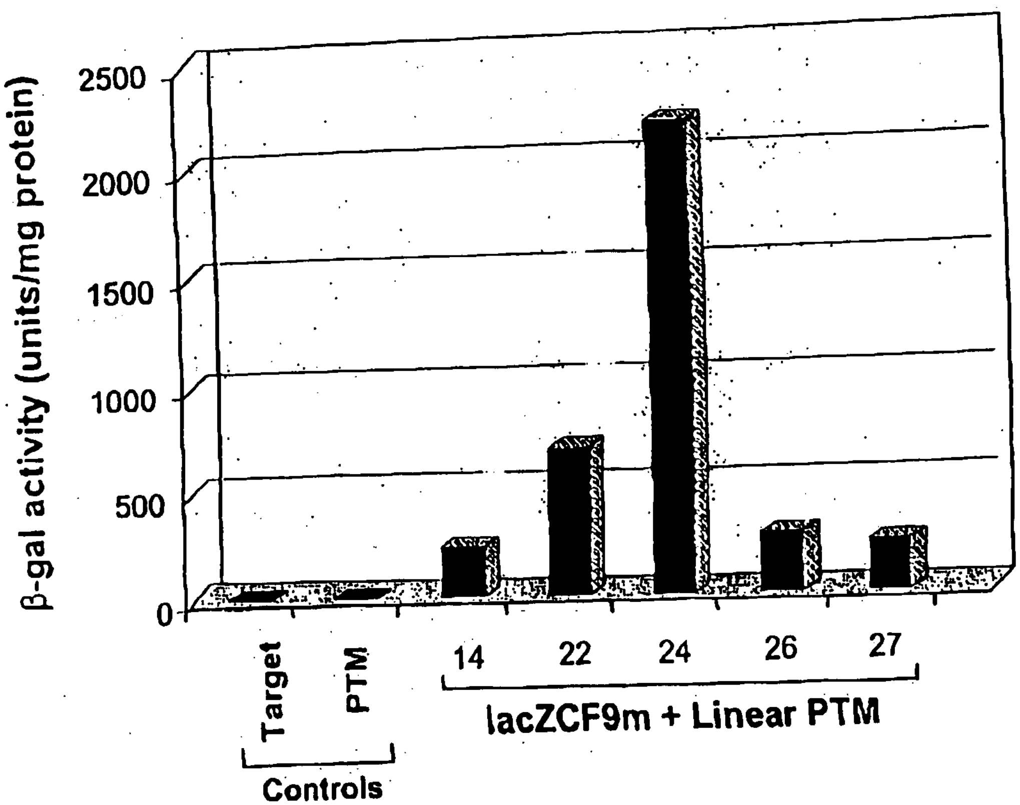


Figure 40B

C

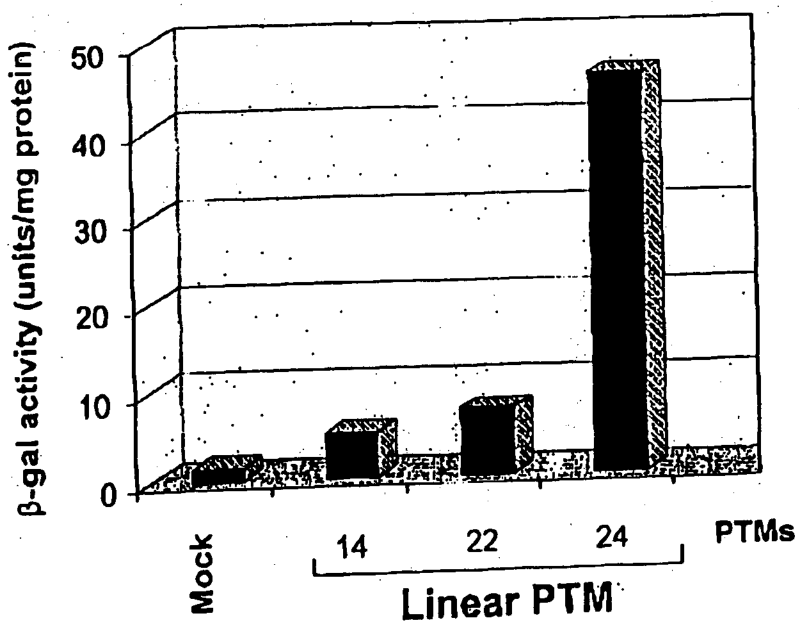

β-gal activity (units/mg protein)
50
40
30
20
10
0
Mock
14
22
24
PTMs
Linear PTM

Figure 40C

A

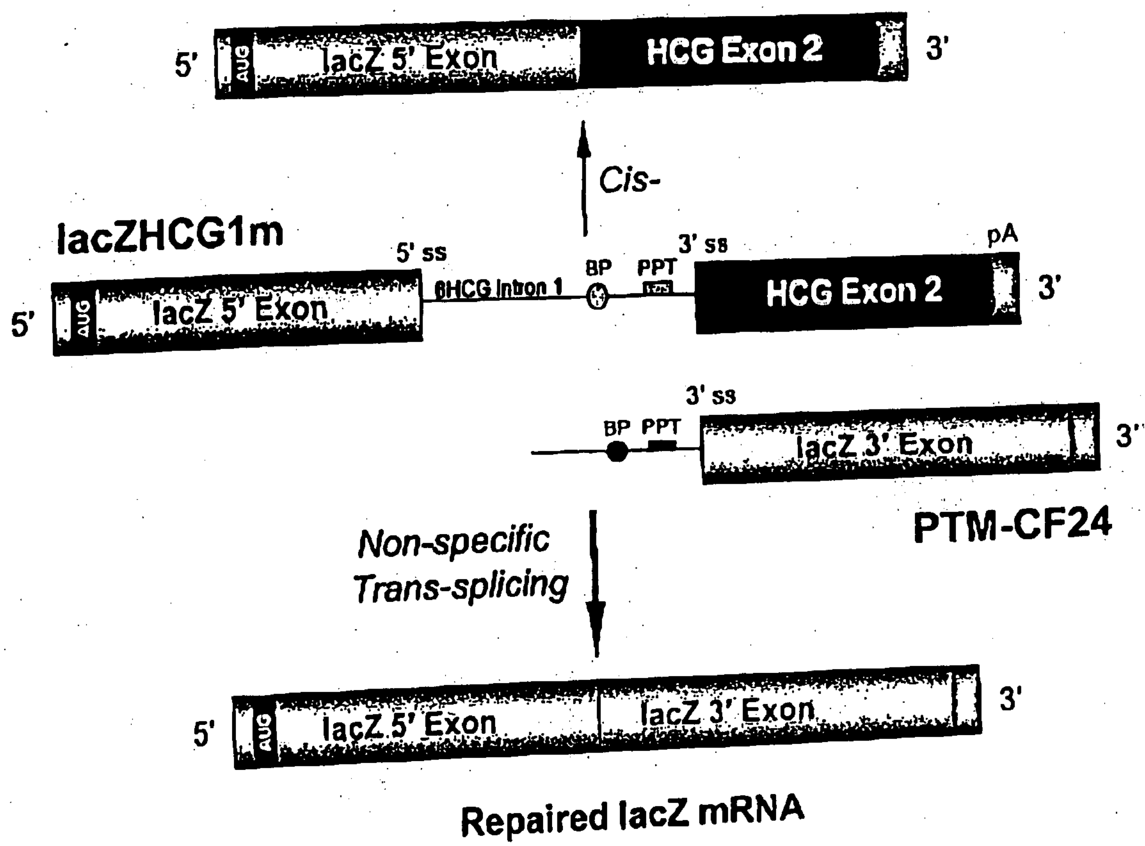

5'
AUG
lacZ 5' Exon
HCG Exon 2
3'
Cis-
lacZHCG1m
5' ss
6HCG Intron 1
BP
PPT
3' ss
pA
5'
AUG
lacZ 5' Exon
HCG Exon 2
3'
3' ss
BP
PPT
lacZ 3' Exon
3'
PTM-CF24
Non-specific
Trans-splicing
5'
AUG
lacZ 5' Exon
lacZ 3' Exon
3'
Repaired lacZ mRNA

Figure 41A

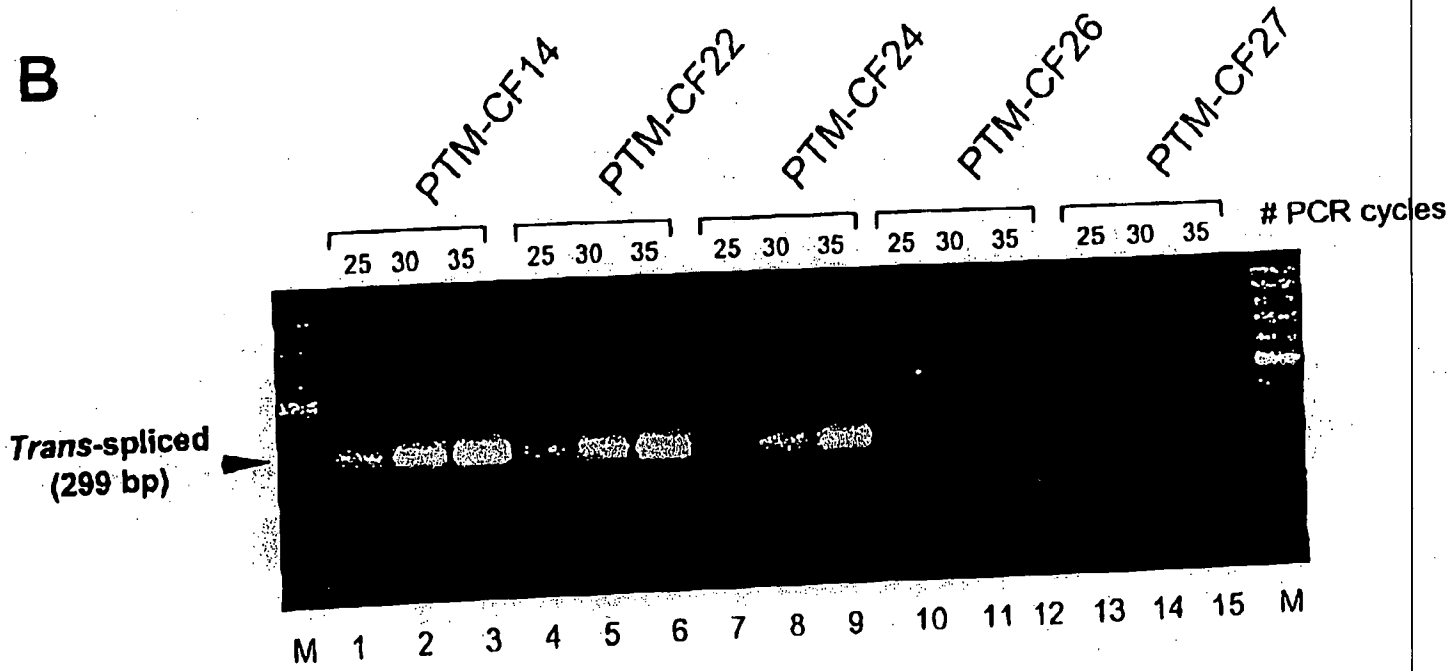


Figure 4B

C

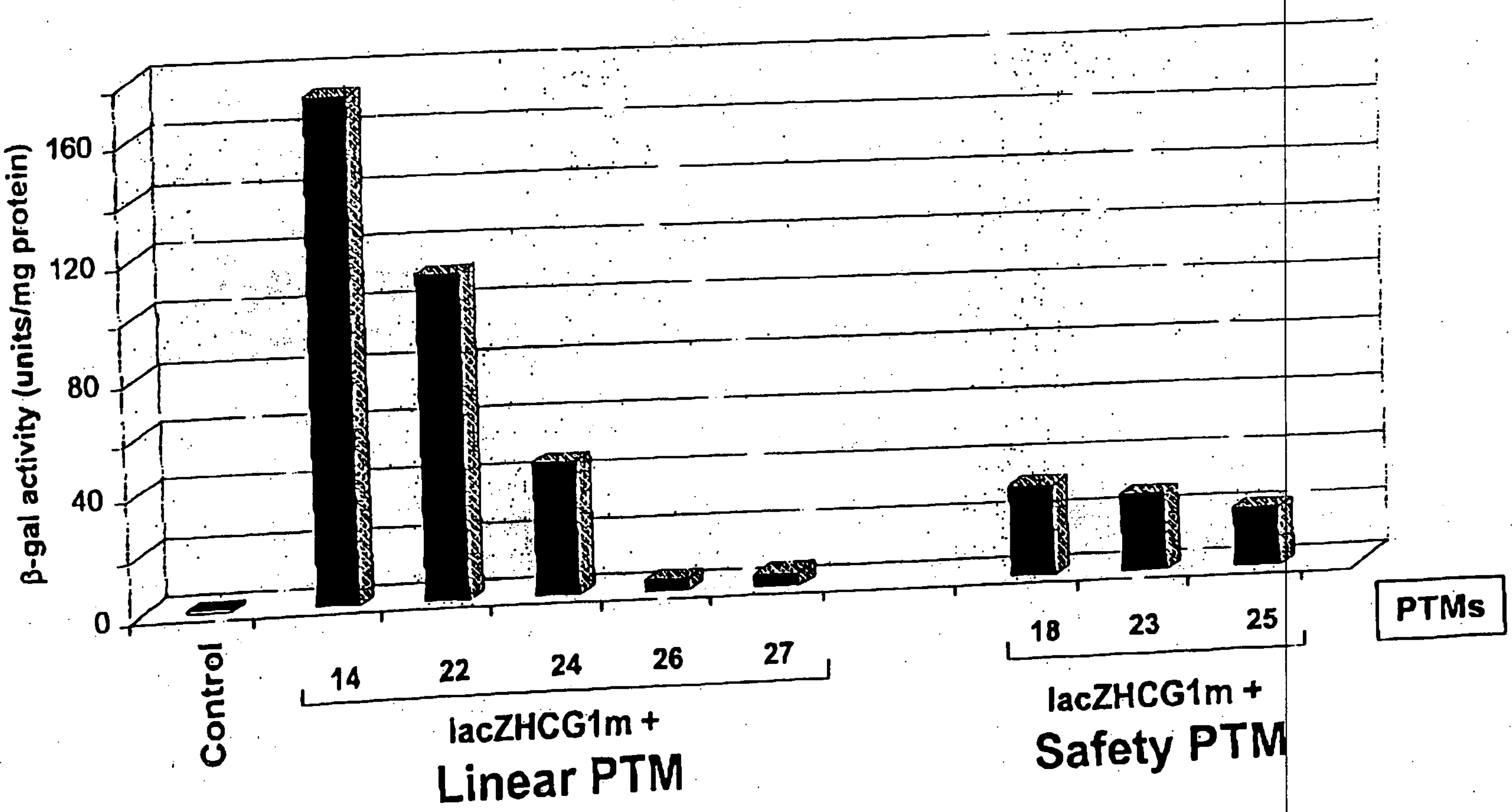

β-gal activity (units/mg protein)
160
120
80
40
0
Control
14
22
24
26
27
lacZHCG1m +
Linear PTM
18
23
25
lacZHCG1m +
Safety PTM
PTMs

Figure 41C

Exons 1-10
ATGCAGAGGTCGCCTCTGGAAAAGGCCAGCGTTGTCTCCAAACTTTTTTCAGCTGGACCAGACCAATTTTGAGGAAAG
GATACAGACAGCGCCTGGAATTGTCAGACATATACCAAATCCCTTCTGTTGATTCTGCTGACAATCTATCTGAAAAATT
GGAAAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAACTCATTAATGCCCTTCGGCGATGTTTTTTCTGG
AGATTTATGTTCTATGGAATCTTTTTATATTTAGGGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCA
~~TAGCTTCCTATGACCCGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTTTAT~~
TGTGAGGACACTGCTCCTACACCCAGCCATTTTTGGCCTTCATCACATTGGAATGCAGATGAGAATAGCTATGTTTAGT
TTGATTTATAAGAAGACTTTAAAGCTGTCAAGCCGTGTTCTAGATAAAATAAGTATTGGACAACTTGTTAGTCTCCTTT
CCAACAACCTGAACAAATTTGATGAAGGACTTGCATTGGCACATTTCGTGTGGATCGCTCCTTTGCAAGTGGCACTCCT
CATGGGGCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTGGACTTGGTTTCCTGATAGTCCTTGCCCTTTTTCAG
GCTGGGCTAGGGAGAATGATGATGAAGTACAGAGATCAGAGAGCTGGGAAGATCAGTGAAAGACTTGTGATTACCTCAG
AAATGATCGAGAACATCCAATCTGTTAAGGCATACTGCTGGGAAGAAGCAATGGAAAAAATGATTGAAAACTTAAGACA
AACAGAACTGAAACTGACTCGGAAGGCAGCCTATGTGAGATACTTCAATAGCTCAGCCTTCTTCTTCTCAGGGTTCTTT
GTGGTGTTTTTATCTGTGCTTCCCTATGCACTAATCAAAGGAATCATCCTCCGGAAAATATTCACCACCATCTCATTCT
GCATTGTTCTGCGCATGGCGGTCACTCGGCAATTTCCCTGGGCTGTACAAACATGGTATGACTCTCTTGGAGCAATAAA
CAAAATACAGGATTTCTTACAAAAGCAAGAATATAAGACATTGGAATATAACTTAACGACTACAGAAGTAGTGATGGAG
AATGTAACAGCCTTCTGGGAGGAGGGATTTGGGGAATTATTTGAGAAAGCAAAACAAAACAATAACAATAGAAAAACTT
CTAATGGTGATGACAGCCTCTTCTTCAGTAATTTCTCACTTCTTGGTACTCCTGTCCTGAAAGATATTAATTTCAAGAT
AGAAAGAGGACAGTTGTTGGCGGTTGCTGGATCCACTGGAGCAGGCAAGA**CGAGCT**T**GC**T**C**ATGATGAT**C**ATGGG**C**GA**G**
TT**A**GA**ACCAAGT**GA**A**GG**C**AA**G**AT**C**AA**A**CA**TTCC**GG**CC**G**C**AT**CAGC**TT**T**G**CAGC**CA**A**TT**CAGTT**GGAT**C**ATGCC**C**GG**T**A
CCAT**C**AA**G**GA**G**AA**C**AT**A**AT**C***TT***C*GG**C**GT**CAGTTAC**GA**C**GA**G**TA**CC**G**C**TA**TC**G**CTCG**GT**G**AT**T**AA**G**GC**C**TG**TCAGTTG**GA
GGAG
Trans-splicing domain
GTAAGATATCACCGATATGTGTCTAACCTGATTCGGGCCTTCGATACGCTAAGATCCACCGG
TCAAAAAGTTTTCACATAATTTCTTACCTCTTCTTGAATTCATGCTTTGATGACGCTTCTGTATCTATATTCATCATTG
GAAACACCAATGATATTTTCTTTAATGGTGCCTGGCATAATCCTGGAAAACTGATAACACAATGAAATTCTTCCACTGT
GCTTAATTTTACCCTCTGAATTCTCCATTTCTCCCATAATCATCATTACAACTGAACTCTGGAAATAAAACCCATCATT
ATTAACTCATTATCAAATCACGCT

Figure 42

153 bp PTM24 Binding Domain:

Nhe I 153 bp BD underlined

GCTAGC-AATAATGACGAAGCCGCCCCTCACGCTCAGGATTCACTTGCCTCCAATTATCATCCTAAGCAGAAGTGTATA

TTCTTATTTGTAAAGATTCTATTAACTCATTTGATTCAAAATATTTAAAATACTTCCTGTTTCACCTACTCTGCTATGC

Sac II

AC-**CCGCGG**

Figure 43A

Trans-splicing domain
AATAATGACGAAGCCGCCCCTCACGCTCAGGATTCACTTGCCCTCCAATTATCATCCTAAGCAGAAGTGTATATTCTTA
TTTGTAAAGATTCTATTAACTCATTTGATTCAAAATATTTAAAATACTTCCTGTTTCACCTACTCTGCTATGCACCCGC
GGAACATTATTATAACGTTGCTCGAATACTAACTGGTACCTCTTCTTTTTTTTTGATATCCTGCAG
Exons 10-24
ACTTCACTTCTAATGATGATTATGGGAGAACTGGAGCCTTCAGAGGGTAAAATTAAGCACAGTGGAAGAATTTCATTCT
GTTCTCAGTTTTCCTGGATTATGCCTGGCACCATTAAAGAAAATATCATCTTTGGTGTTTCCTATGATGAATATAGATA
CAGAAGCGTCATCAAAGCATGCCAACTAGAAGAGGACATCTCCAAGTTTGCAGAGAAAGACAATATAGTTCTTGGAGAA
GGTGGAATCACACTGAGTGGAGGTCAACGAGCAAGAATTTCTTTAGCAAGAGCAGTATACAAAGATGCTGATTTGTATT
TATTAGACTCTCCTTTTGGATACCTAGATGTTTTAACAGAAAAAGAAATATTTGAAAGCTGTGTCTGTAAACTGATGGC
TAACAAAACTAGGATTTTGGTCACTTCTAAAATGGAACATTTAAAGAAAGCTGACAAAATATTAATTTTGCATGAAGGT
AGCAGCTATTTTTATGGGACATTTTCAGAACTCCAAAATCTACAGCCAGACTTTAGCTCAAAACTCATGGGATGTGATT
CTTTCGACCAATTTAGTGCAGAAAGAAGAAATTCAATCCTAACTGAGACCTTACACCGTTTCTCATTAGAAGGAGATGC
TCCTGTCTCCTGGACAGAAACAAAAAAACAATCTTTTAAACAGACTGGAGAGTTTGGGGAAAAAAGGAAGAATTCTATT
CTCAATCCAATCAACTCTATACGAAAATTTTCCATTGTGCAAAAGACTCCCTTACAAATGAATGGCATCGAAGAGGATT
CTGATGAGCCTTTAGAGAGAAGGCTGTCCTTAGTACCAGATTCTGAGCAGGGAGAGGCGATACTGCCTCGCATCAGCGT
GATCAGCACTGGCCCCACGCTTCAGGCACGAAGGAGGCAGTCTGTCCTGAACCTGATGACACACTCAGTTAACCAAGGT
CAGAACATTCACCGAAAGACAACAGCATCCACACGAAAAGTGTCACTGGCCCCTCAGGCAAACTTGACTGAACTGGATA
TATATTCAAGAAGGTTATCTCAAGAAACTGGCTTGGAAATAAGTGAAGAAATTAACGAAGAAGACTTAAAGGAGTGCTT
TTTTGATGATATGGAGAGCATACCAGCAGTGACTACATGGAACACATACCTTCGATATATTACTGTCCACAAGAGCTTA
ATTTTTGTGCTAATTTGGTGCTTAGTAATTTTTCTGGCAGAGGTGGCTGCTTCTTTGGTTGTGCTGTGGCTCCTTGGAA
ACACTCCTCTTCAAGACAAAGGGAATAGTACTCATAGTAGAAATAACAGCTATGCAGTGATTATCACCAGCACCAGTTC
GTATTATGTGTTTTACATTTACGTGGGAGTAGCCGACACTTTGCTTGCTATGGGATTCTTCAGAGGTCTACCACTGGTG
CATACTCTAATCACAGTGTCGAAAATTTTACACCACAAAATGTTACATTCTGTTCTTCAAGCACCTATGTCAACCCTCA
ACACGTTGAAAGCAGGTGGGATTCTTAATAGATTCTCCAAAGATATAGCAATTTTGGATGACCTTCTGCCTCTTACCAT
ATTTGACTTCATCCAGTTGTTATTAATTGTGATTGGAGCTATAGCAGTTGTCGCAGTTTTACAACCCTACATCTTTGTT
GCAACAGTGCCAGTGATAGTGGCTTTTATTATGTTGAGAGCATATTTCCTCCAAACCTCACAGCAACTCAAACAACTGG
AATCTGAAGGCAGGAGTCCAATTTTCACTCATCTTGTTACAAGCTTAAAAGGACTATGGACACTTCGTGCCTTCGGACG
GCAGCCTTACTTTGAAACTCTGTTCCACAAAGCTCTGAATTTACATACTGCCAACTGGTTCTTGTACCTGTCAACACTG
CGCTGGTTCCAAATGAGAATAGAAATGATTTTTGTCATCTTCTTCATTGCTGTTACCTTCATTTCCATTTTAACAACAG
GAGAAGGAGAAGGAAGAGTTGGTATTATCCTGACTTTAGCCATGAATATCATGAGTACATTGCAGTGGGCTGTAAACTC
CAGCATAGATGTGGATAGCTTGATGCGATCTGTGAGCCGAGTCTTTAAGTTCATTGACATGCCAACAGAAGGTAAACCT
ACCAAGTCAACCAAACCATACAAGAATGGCCAACTCTCGAAAGTTATGATTATTGAGAATTCACACGTGAAGAAAGATG
ACATCTGGCCCTCAGGGGGCCAAATGACTGTCAAAGATCTCACAGCAAAATACACAGAAGGTGGAAATGCCATATTAGA
GAACATTTCCTTCTCAATAAGTCCTGGCCAGAGGGTGGGCCTCTTGGGAAGAACTGGATCAGGGAAGAGTACTTTGTTA
TCAGCTTTTTTGAGACTACTGAACACTGAAGGAGAAATCCAGATCGATGGTGTGTCTTGGGATTCAATAACTTTGCAAC
AGTGGAGGAAAGCCTTTGGAGTGATACCACAGAAAGTATTTATTTTTTCTGGAACATTTAGAAAAAACTTGGATCCCTA
TGAACAGTGGAGTGATCAAGAAATATGGAAAGTTGCAGATGAGGTTGGGCTCAGATCTGTGATAGAACAGTTTCCTGGG
AAGCTTGACTTTGTCCTTGTGGATGGGGGCTGTGTCCTAAGCCATGGCCACAAGCAGTTGATGTGCTTGGCTAGATCTG
TTCTCAGTAAGGCGAAGATCTTGCTGCTTGATGAACCCAGTGCTCATTTGGATCCAGTAACATACCAAATAATTAGAAG
AACTCTAAAACAAGCATTTGCTGATTGCACAGTAATTCTCTGTGAACACAGGATAGAAGCAATGCTGGAATGCCAACAA
TTTTTGGTCATAGAAGAGAACAAAGTGCGGCAGTACGATTCCATCCAGAAACTGCTGAACGAGAGGAGCCTCTTCCGGC
AAGCCATCAGCCCCTCCGACAGGGTGAAGCTCTTTCCCCACCGGAACTCAAGCAAGTGCAAGTCTAAGCCCCAGATTGC
Histidine tag Stop
TGCTCTGAAAGAGGAGACAGAAGAAGAGGTGCAAGATACAAGGCTTCATCATCATCATCATCATTAG

Figure 43B

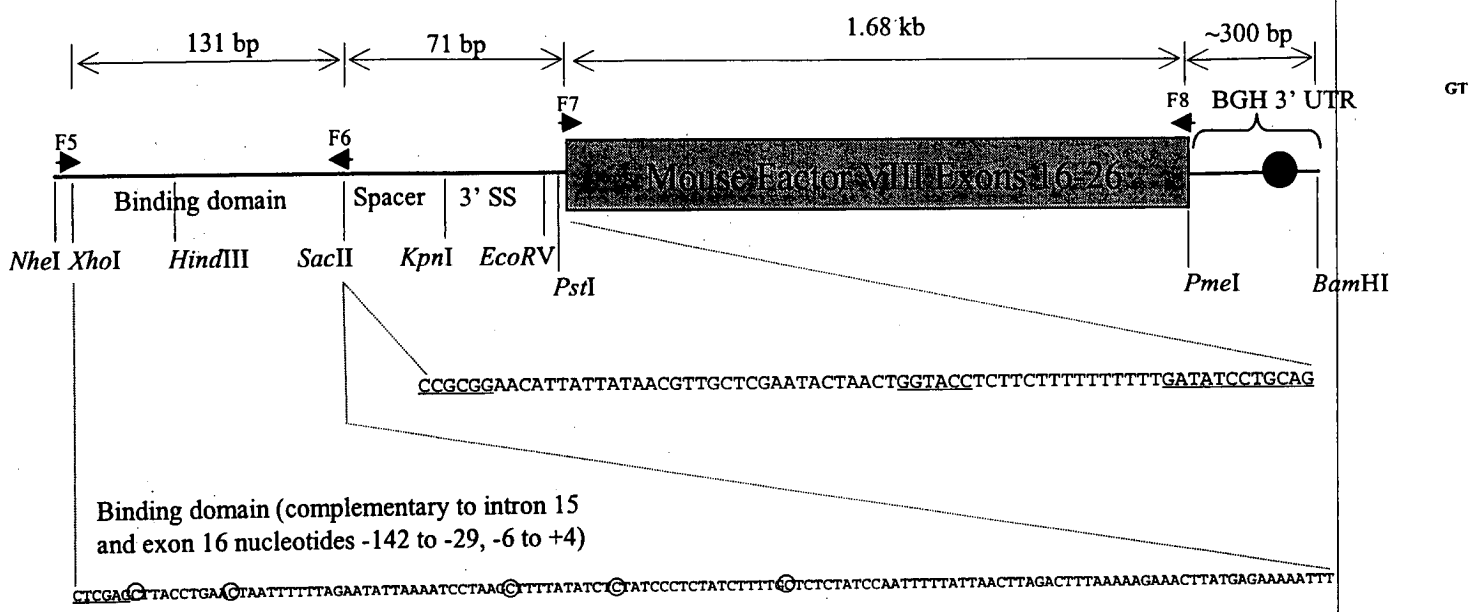


Figure 44A

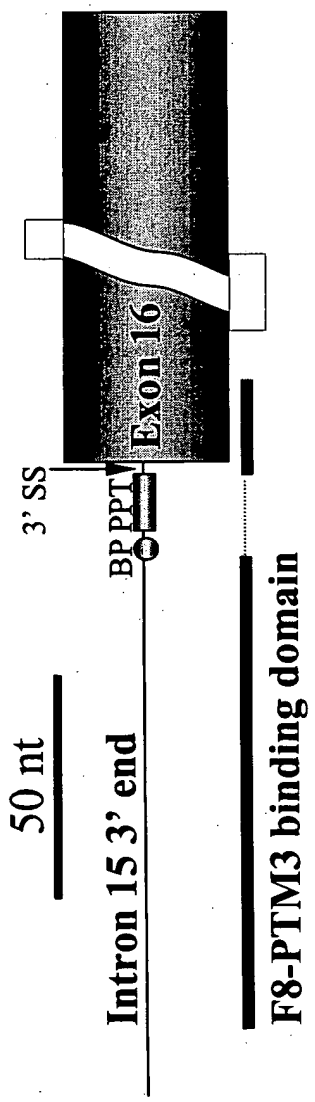


Figure 44 B

Figure 44C

NcoI
CCATGGTCGACGTTAGCCCCACGTTCTGCTTCACTCTCCCCATCTCCCCCCCCCTCCCCACCCCCAATT

TTGTATTTATTTATTTTTTAATTATTTTGTGCAGCGATGGGGGCGGGGGGGGGGGGGGGGCGCGCGCCAGGC

GGGGCGGGGCGGGGCGAGGGGCGGGGCGGGGCGAGGCGGAGAGGTGCGGCGGCAGCCAATCAGAGCGGCGCG

CTCCGAAAGTTTCCTTTTATGGCGAGGCGGCGGCGGCGGCGGCCCTATAAAAAGCGAAGCGCGCGGCGGGCG

F13
GGAGTCGCTGCGACGCTGCCTTCGCCCCGTGCCAACCTCCGCCTCGAGCTTACCTGAACTAATTTTTTAGAA

HindIII
TATTAAAATCCTAAGCTTTTATATCTCTATCCCTCTATCTTTTGCTCTCTATCCAATTTTTATTAACTTAGA

SacII
CTTTAAAAAGAAACTTATGAGAAAAATTTCCGCGGAACATTATTATAACGTTGCTCGAATACTAACTGGTAC

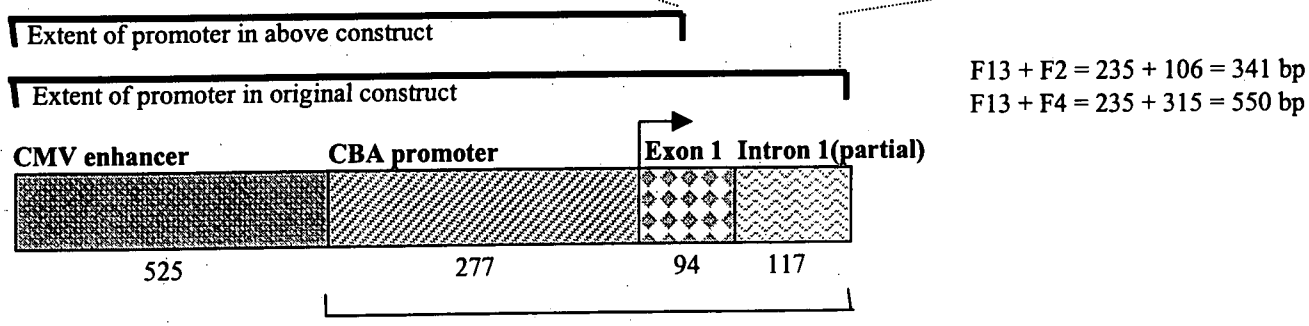
EcoRV PstI
CTCTTCTTTTTTTTTTTGATATCCTGCAG

Chicken β-actin Promoter

Nucleotide changes are shown in blue
Boxed = CAT box, TATA box
Boxed + Arrow = Transcription Start
Oval = Downstream elements
Bold = Binding domain
Italicized = Spacer+PPT+BP+AG dinucleotide

Sequence not included in construct

CGCCGCCTCGCGCCGCCCGCCCCGGCTCTGACTGACCGCGTTACTCCCACAGGTGAG
CGGGCGGGACGGCCCTTCTCCTCCGGGCTGTAATTAGCGCTTGGTTTAATGACGGCT
TGTTTCTTTTCTGTGGCTGCGTGAAAGCCTTGAGGGGCTCCGGGAGGAATTCGTA



F13 + F2 = 235 + 106 = 341 bp
F13 + F4 = 235 + 315 = 550 bp

Chicken Beta Actin Promoter (including exon 1 and part of intron 1)

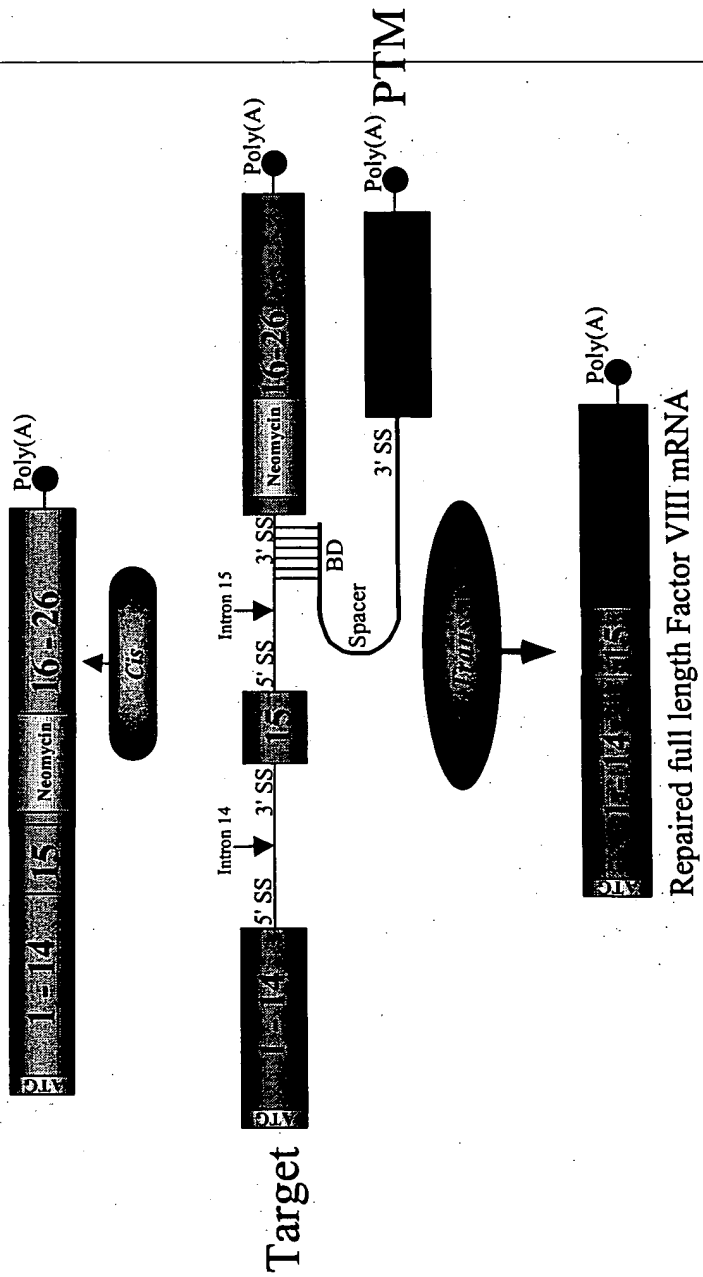
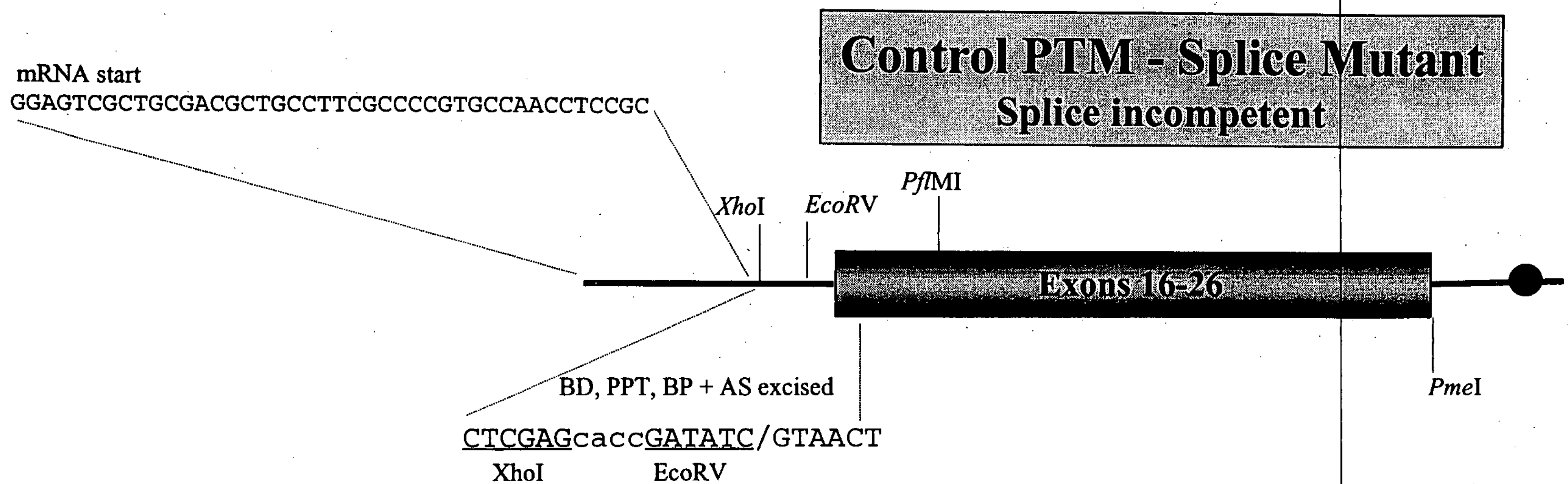

Poly(A)
ATG
1-14
15
Neomycin
16-26
Cis
Poly(A)
Intron 14
5' SS
3' SS
Intron 15
5' SS
3' SS
BD
Spacer
Poly(A)
PTM
3' SS
Poly(A)
Repaired full length Factor VIII mRNA
Target

Figure 44D

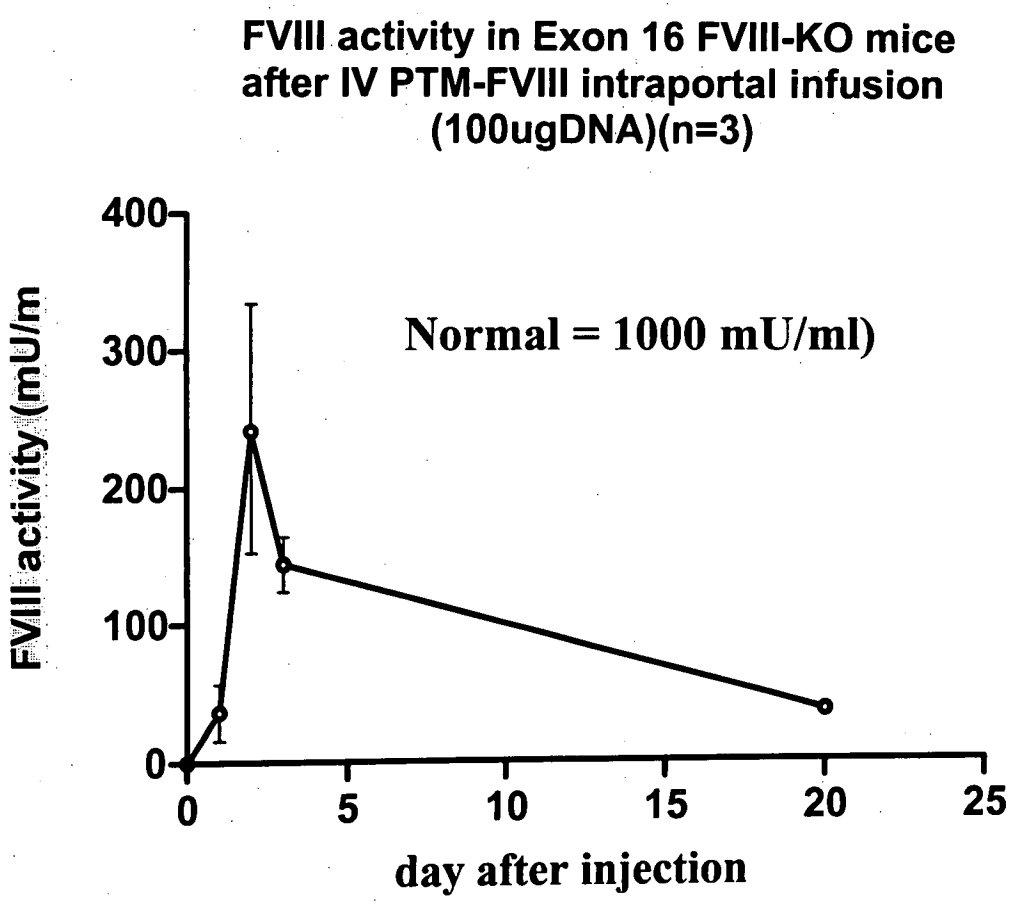
Figure 45



Method:
Excise TSD and part of exon 16 with XhoI and PflMI and ligate in a PCR product that:
1) eliminates the TSD and splice acceptor site
2) inserts EcoRV adjacent to exon 16
3) restores the coding for exon 16

Repair of Factor VIII

Preliminary results from one experiment



METHODS

Inject plasmid intraportally

↓

Sample blood (1, 2, 3, 20 d)

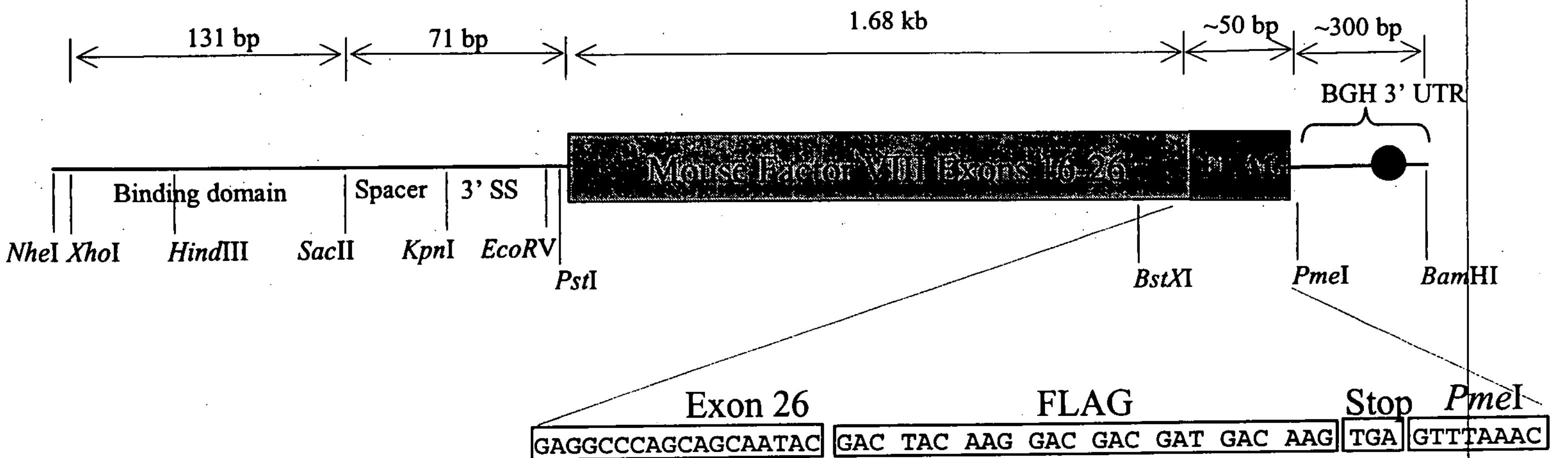
↓

Assay for factor VIII activity

(shut 64 of 66)

Figure 46

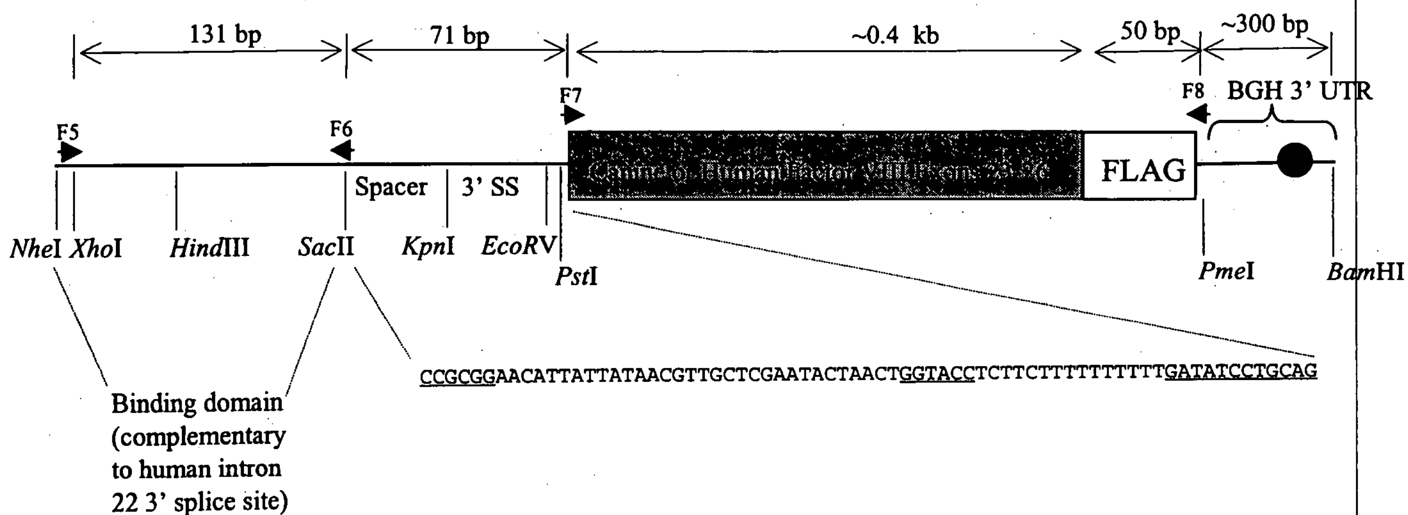
Detailed structure of a mouse factor VIII PTM containing normal sequences for exons 16-26 and a C-terminal FLAG tag. BGH = bovine growth hormone 3' UTR; Binding domain = 125 bp.



REFERENCE FOR DESIGN OF FLAG TAG

Brann T, Kayda D, Lyons RM, Shirley P, Roy S, Kaleko M, Smith T.
Adenoviral vector-mediated expression of physiologic levels of human factor VIII in nonhuman primates.
Hum Gene Ther 1999 Dec 10;10(18):2999-3011
Genetic Therapy, Inc., a Novartis Company, Gaithersburg, MD 20878, USA.
Epitope-tagged B domain-deleted human factor VIII cDNA (flagged FVIII) was evaluated in nonhuman primates.

Figure 47A



FLAG = C-terminal tag to be used to detect repaired factor VIII protein.

Figure 47B